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30-APR-1998 AAW33698;

(first entry)

AAW33698 standard; protein; 455 AA.

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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-1996;
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te= "mature protein"
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Human AL-2 neurotrophic factor and related DNA - used to develop products for, e.g. treating neurologic disorders, angiogenesis disorders, tumours or rheumatoid arthritis or for wound healing.

N-PSDB; AAV06354.

Claim 20;

Fig

1A-C; 86pp; English.

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(first entry)
                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2450; DB 2;
100.0%; Pred. No. 3.6e-197;
tive 0; Mismatches 0;
                                                                                                340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                               The amino acid sequence was deduced from a human foetal brain cDNA clone (C (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk, C which are members of the eph/elk family of receptor tyrosine kinases. CC Lerk-8 polypeptides, especially soluble polypeptides comprising amino CC acid residues -27 to 142-197 of the full-length protein, can be expressed CC in transformed host cells. These polypeptides can be used to purify hek CC or elk proteins, and to purify or identify cells that express hek or elk CC on the surface. Such cells can be used in various in vitro studies or in CC vivo procedures, e.g. neural cells expressing elk can be administered to CC a mammal afflicted with a neurodegenerative disorder. The Lerk-8 CC polypeptides can also be used to deliver diagnostic or therapeutic agents CC to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides CC can also be used to: treat disorders mediated by defective or consufficient amounts of Lerk-8; to treat disorders such as injury to contain tissue or neurologic disease; to promote angiogenesis; and for CC wound healing or stimulating neovascularisation of grafted tissues
                                             Query Match
Best Local S
Matches 338
                                                                                                             Sequence 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated cytokine, tyrosine kinases, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cerretti DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          This protein sequence comprises a novel human cytokine designated Lerk-8
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 32-33; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytokine Lerk-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;
neurodegenerative disease; wound healing; neovascularisation; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-503043/46.
                                                                Similarity
MGPPHSGPGGVRVGALLLLGVLGIVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                 Conservative
                                                                                                               A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-00621146.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "residue 325 is Leu in Lerk-8 variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label = Sig_peptide
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                                                            75.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lerk-8 - binds to the hek and elk receptor to develop products for diagnosis and then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "N-glycosylated"
                                               0;
                                             Score 1841; DB 2; 1
Pred. No. 4.1e-146;
0; Mismatches 0;
                                                                             Length 340;
                                                  Indels
                                                 0,
                    60
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LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL

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RESULT 3
ANAW33699
ANAW3699
ANAW369
ANAW
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This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related tyrosine kinase receptor ligand. AL-2 can be administered to patients whom the nervous system has been damaged by trauma, surgery, stroke, ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents, to promote the survival or growth of neurons. They can be used to treat motoneuron disorders such as
                                                                                                                                                                                                                           Human AL-2 neurotrophic factor and related DNA - used for, e.g. treating neurologic disorders, angiogenesis or rheumatoid arthritis or for wound healing.
                                                                                                                                                                                                                                                                                                                           WPI; 1997-535837/49.
N-PSDB; AAV06355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour; rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia; psoriasis; Alzheimer's disease; epilepsy.
                                                                                                                                                                             Claim 20; Fig 2A-B; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
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220. .245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                       to develop products disorders, tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 338; Conserv
                                                                                                                                                                                                                                                                                                                                  LERK; ligand for eph-related kinase; ERK; NLERK2; receptor protein tyrosine kinase; cell proliferation; cell differentiation; cell survival; nerve cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW10637 standard;
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                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLERK2 ligand for eph-related kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1997
                                                                         Protein
                                                                                                                                               Peptide
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/label=_Sig_peptide
                                                                                                                                                                                      Location/Qualifiers
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label= 1
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                                      Mat_protein
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27-NOV-1995;
22-DEC-1995;
05-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel human ligand for eph-related kinase (LERK) is designated NLERK2 (AAW10637). It is encoded by a cDNA (clone (AAF60966) obtd. from a human foetal brain cDNA library. The novel receptor ligand can be expressed in transformed host cells and used in methods for regulating the development, maintenance or regeneration of different cells (e.g. neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be used to treat injury, disease or abnormality in the nervous system, and membrane-bound NLERK2 to modulate proliferation, different or survival e.g. in grafting procedures or transplantation. NLERK2 can also be used to raise antibodies for use in immunotherapy, and to detect anti-NLERK2 antibodies that may occur in some autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid mol. encoding ligand for eph-related kinase - useful for treatment of, pref. neuronal, cells to increase survival, proliferation and differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 37-39; 71pp; English
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N-PSDB; AAT60966.
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                 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                                                                           GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
                                                                                                                                       VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                    SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                                                          GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
                                                                                                                                                                                 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
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                                                                                                                      VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
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95AU-00006847.
95AU-00007299.
96AU-00007890.
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                                                                                                                                                                                                                                                                                                                                                                  Score 1841; DB 2; 1
Pred. No. 4.1e-146;
0; Mismatches 0;
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RESULT 5 ABU07845

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SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP

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                                                                                                                                                                                                                                     The invention describes a method of identifying a modulator of binding CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method CC composition in the presence and in the absence of a putative modulator CC composition in the presence and in the absence of a putative modulator CC in the presence and in the absence of the putative modulator. The method CC is useful for identifying a modulator of binding between a Tie receptor CC tyrosine kinase and an Ephrin ligand. Modulators identified from the CC method are useful in modulating angiogenic processes, including CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-CC Tie biology, aberrant growth, migration or proliferation of cells that CC express a Tie receptor, or for promoting growth of vessel or CC chronic compound, or a tissue graft or transplant). This is the amino CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of CC ligands that are bound to the membrane via a transmembrane domain and CC short cytoplasmic tail and function as Eph receptor ligands
                                                                                                                                       Query Match
Best Local S
Matches 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ligand-receptor binding modulator; ephrin ligand; anglogenesis; lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder; cell migration disorder; cell proliferation disorder; neovascularisation; ischaemia; infarction; tissue graft; transplant; human; ephrin-B3; tie receptor tyrosine kinase; Eph receptor ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of a putative
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 117-119; 199pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alitalo K, Kubo H;
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                                                                                                                                                         Similarity
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                     LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                   MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                         Conservative
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                                                                                                                                                        75.1%;
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                                                                                                                                                        Score 1841; DB 6; I
Pred. No. 4.1e-146;
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RESULT 6
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                                       S
                                                                                                                 Query Match
Best Local S
Matches 338
                                                                                                                                                                                                                                                                                    The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression in the first soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma—upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 4256; 210pp; English.
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                                                                                                                                             Local Similarity
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   MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                                                                    Conservative
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                                                                                                     75.1%; bul
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zlotník A;
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                                                                                                                 Score 1841; DB 8; 1
Pred. No. 4.1e-146;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; vaccine;
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                                                                 The invention relates to a novel use of ephrin, ephrin inhibitors, and ephrin receptors for alleviating a symptom of a disorder having reduced ephrin receptors for alleviating a symptom of a disorder having reduced levels of hematopoiesis, having increased levels of cellular proliferation in an intestinal tract, or having an abnormal level of cellular proliferation in a tissue. A composition of the invention has cytostatic, antianemic, antianemic
                                                                                                                                                                                                                                                                                                             Use of ephrin and its molecules for alleviating a symptom or a dison with reduced levels of hematopoiesis, increased levels of cellular proliferation in an intestinal tract, or abnormal level of cellular proliferation in a tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2001; 2001US-0345206P.
02-JUL-2002; 2002US-0393272P.
08-NOV-2002; 2002US-00291290.
03-APR-2003; 2003US-046048BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic;
antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatological;
                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 16; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-195317/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FRIS/)
(HOLM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coagulant; immunostimulant; cerebroprotective; vasotropic; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ephrin-B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-2005
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                      wasotropic, and a
murine ephrin-B3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRISEN J.
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New nucleic acid encoding Ef1-6 ligand protein growth and proliferation of neuronal cells and
                                                                                                                                                                                                                                                                                                                                                                Efl-6; Eph; Elk; rece
neurological disease.
                                    WPI; 1997-259021/23.
N-PSDB; AAT69808.
                                                                                                                                                                                                                                                          Misc-difference
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                                                                       Davis S,
                                                                                                                        25-OCT-1995;
                                                                                                                                               25-OCT-1996;
                                                                                                                                                                                                                                                                                 Protein
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                                                                         Gale
                                                                                                                                                                                                                                                                                                                                                                              Elk; receptor tyrosine kinase; signal transduction; ligand;
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                                                                         WW,
                                                                                                                        95US-0007015P
                                                                                                                                               96WO-US017201
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                            /label= Gln,
                                                                                                                                                                                                                                                                    /label= Mat_protein
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Pred. No. 4.1e-146;
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    used for promoting
in drug screening.

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel ligand (AAW17081), designated Ef1-6 (or Eph transmembrane tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4, Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6, truncated soluble polypeptides comprising the extracellular domain of Elf-6, and Ef1-6 ligandbodies comprising soluble Ef1-6 and the Fc portion of IgG can be expressed in host cells. These can be used to support neuronal and other Eph receptor-bearing cell populations for treatment of the receptor-bearing cell populations for treatment of the receptor in drug accepting and to raise diagnostic
                                                                                                                                                                                                                             Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand; human; signal transduction; axonogeness; nerve cell; neurone; hlzheimer; disease; parkinson's disease; Huntingdon's disease; demyelination; multiple sclerosis; amyotrophic lateral sclerosis; nervous system infection; Wernicke's disease; trauma; ischaemia; st
                                                                                                                                                                         nutritional polyneuropathy; progressive supranuclear palsy; Shy Drager's syndrome; multistem degeneration; olivo ponto cerebellar atrophy, peripheral nerve damage.
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                                                     Domain
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                                                                                      Location/Qualifiers
                                                 'label= Gln, Arg
25. .249
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99.7%;
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Pred. No. 1.3e-145;
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                                      domain"
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301

GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIYY 338

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CC ligand comprises forming a complex between a purified and isolated CC oligomerised ERRTK, or an isoform or an extracellular domain of the CC ERRTK, and the transmembrane ligand expressed on the cell. The complex CC can also be used for evaluating a substance for its ability to modulate the biological activity of a transmembrane ligand for an ERRTK, and to CC identify substances that affect or modulate a pathway regulated by a CC ERRTK. A purified and isolated oligomerised ERRTK can be used in the CC preparation of a medicament for modulating neuronal development or CC regeneration in a subject, or in a medicament for modulating axonogenesis in a subject (all claimed). The substances identified by the methods can be used to modulate axonogenesis, nerve cell interactions and CC regeneration, to treat diseases and conditions involving trauma and CC regeneration, to treat diseases and conditions involving trauma and CC disease, Huntingdon's disease, demyelinating diseases, such as multiple CC disease, mayotrophic lateral sclerosis, bacch as Mernicke's disease CC of the nervous system, deficiency diseases, such as Mernicke's disease CC and nutritional polyneuropathy, progressive supranuclear paley, Shy CC Drager's syndrome, multistem degeneration and olivo ponto cerebellar CC atrophy, peripheral nerve damage, trauma, and ischaemia resulting from cracky.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOUN ) MOUNT SINAI HOSPITAL CORP
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GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIXY 338
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                                                                                                                                                                      GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
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99.4%;
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Pred. No. 6.2e-145;
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RESULT 10
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ID ABU07846
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)B; ABX12547.
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Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of a putative

Disclosure; Page 121-122; 199pp; English

composition in the presence and in the absence of a putative modulator compound, and detecting the binding between Tie receptor and the Ephrin in the presence and in the absence of the putative modulator. The method is useful for identifying a modulator of binding between a Tie receptor tyrosine kinase and an Ephrin ligand. Modulators identified from the method are useful in modulating angiogenic processes, including lymphangiogenesis, for treating diseases associated with aberrant Ephrin-Tie biology, aberrant growth, migration or proliferation of cells that express a Tie receptor, or for promoting growth of vessel or neovascularisation (e.g. ischaemic tissue, an infarction, a new or chronic compound, or a tissue graft or transplant). This is the amino acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of ligands that are bound to the membrane via a transmembrane domain and short cytoplasmic tail and function as Eph receptor ligands The invention describes a method of identifying a modulator of between a Tie receptor tyrosine kinase and an Ephrin ligand. The comprises contacting a Tie receptor composition with an Ephrin of binding The method

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Gaps

Sequence 340 AA;

180

120

60

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                                                                            Query Match
Best Local S
Matches 323
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                                                                                           Similarity
                                        MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
                           MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                               Conservative
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95.6%;
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                     The invention relates to a novel use of ephrin, ephrin inhibitors, and ephrin receptors for alleviating a symptom of a disorder having reduced levels of hematopolesis, having increased levels of cellular proliferation in an intestinal tract, or having an abnormal level of cellular proliferation in a tissue. A composition of the invention has cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal egen., dermatological, coagulant, immunostimulant, cerebroprotective, vasotropic, and antiulcer activity. The present sequence represents murine ephrin-B3.
                                                                                                                                                                                      Use of ephrin and its molecules for alleviating a symptom or a disorder with reduced levels of hematopoiesis, increased levels of cellular proliferation in an intestinal tract, or abnormal level of cellular proliferation in a tissue.
                                                                                                                                                                                                                                                                                                                                                      09-NOV-2001; 2001US-0345206P.
02-JUL-2002; 2002US-0393272P.
08-NOV-2002; 2002US-00291290.
03-APR-2003; 2003US-0460488P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic; antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatolog coagulant; immunostimulant; cerebroprotective; vasotropic; antiulc
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                                                                                                                                                             Disclosure; SEQ ID NO 8; 68pp; English.
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HOLMBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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Best Local S
Matches 323
                                           Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correl with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic spilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; notropic; antidiabetic; anticonvulsant; antia osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                           Ghosh SS,
Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                         12-APR-2002; 2002US-0372843P
17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
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Pred. No. 3.2e
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction; organogenesis; oncogenesis; tumour; neurological disorder; diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Eph receptor ligand ELF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW00287 standard; protein;
23-FEB-1996;
                                                          06-SEP-1996
                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy.
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                                                                                                                    WO9626958-A2
                                                                                                                                                                                                                                                                                                                        Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPRKPVSEMEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGI
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   96WO-US002673.
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                                                                                                                                                                           /label=
                                                                                                                                                                                                                               label= Receptor_binding_site
                                                                                                                                                                                                                                                                                         label Extracellular_domain
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                                                                                                                                                                           Transmembrane_domain
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Pred. No. 9.8e-122;
0; Mismatches 0;
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RESULT 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Eph receptor ligand ELF-2 (AAM00287) is strongly expressed in the anterior hindbrain and newly-forming somites of embryos at the early organogenesis stage of development. It is important in cellular communication during pattern formation. Its amino acid sequence was deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain cDNA library. The ELF-2 ligand can be used to alter neurological development, oncogenesis and growth regulation, to modulate binding of ELF-2 to the Eph receptor, and in diagnostic assays
                                            Mus musculus
                                                                                                                 Murine hepatoma transmembrane kinase receptor ligand
                                                                                                                                               21-MAY-1996
                                                                                                                                                                            AAR92742;
                                                                                                                                                                                                          AAR92742 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eph receptor ligand, ELF-2, and DNA encoding it - used prevent neurological diseases, and to modulate binding receptor, e.g. to prevent or treat tumour formation.
                                                                       neurodegenerative
                                                                                     Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 1A-B; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                             YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                                                                                                                                                                       KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                                                                                                    WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                                                                                                                                                                                                 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFÄGIÄSGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                             GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN
                                                                                                                                                                                                                                                                                YEKVSGDYGHPVYIVQEMPPQSPANIYY
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41.8%; Pred. No. 3.8e-44;
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WO9602645-A2

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                          CC activate, the Htk receptor, have been identified in a variety of tissues CC using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the CC using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the CC murine Htk ligand protein following a signal peptide cleavage is 34 kD cc with an estimated pl of 8.9. The murine and human ligands show 96% cc homology at the amino acid level. The DNA is used to produce recombinant CC ligands; for tissue- specific typing (partic. as a marker for breast CC cancer) and as a marker for human chromosome 13. The ligands (partic. in CC soluble form) are used to activate the tyrosine kinase domain of the Htk CC receptor, i.e. to stimulate or inhibit growth, differentiation, and/or activation of cells contg. the receptor, e.g. treatment of neurodegenerative diseases, since they are strongly expressed in the CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are also useful as a control or standard in assays, for generation of CC antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor positive cells, as research agent, in screening, etc
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand for the hepatoma trans-membrane kinase receptor - useful stimulating and inhibiting cells carrying the receptor, e.g. for neuro-degenerative disease.
             ADY51238;
                                    ADY51238
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                         GQYEYYKYYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLMGLEFQKNK 133
                                                                                                                                                                                                                                       DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                             PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
                                                                                                                                                                                                                                                                                                                                         GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                    standard;
                                                                                                       YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                                                                                                                                                                                  GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                     GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                                                                                                                   GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                                                                                                          336 AA;
                                                                                                                                     KYRRRHRKHSPOHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                                                                                                          WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                          YEKVSGDYGHPVYIVQEMPPQSPANIYY 334
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00277722
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                                  protein;
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Pred. No. 3.8e-44;
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                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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02-JUL-2002;
08-NOV-2002;
03-APR-2003;
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(HOLM/)
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The invention relates to a novel use of ephrin, ephrin inhibitors, and ephrin receptors for alleviating a symptom of a disorder having reduced levels of hematopoiesis, having increased levels of cellular proliferation in an intestinal tract, or having an abnormal level of cellular proliferation in a tissue. A composition of the invention has cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal gen, dermatological, coagulant, immunostimulant, cerebroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of ephrin and its molecules for alleviating a symptom or a diswith reduced levels of hematopolesis, increased levels of cellular proliferation in an intestinal tract, or abnormal level of cellular proliferation in a tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vasotropic, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2003; 2003US-00698907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2005049194-A1.
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137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                   DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                     GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                                                                                                                         GLLMVLCRTAISRSIVLEPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFÄGIÄSGCIIFIVIIITLVVLLL
                                                                                                                              GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
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; 2002US-0393272P.
; 2002US-00291290.
; 2003US-0460488P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 628.5; DB 9;
Pred. No. 3.8e-44;
49; Mismatches 129;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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 Score
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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
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1850
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                                                                                                                                                                                                                                                                       Length DB
 GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                            ADJ70889
AAW00287
AAR92742
ADY51238
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ADY51247
AAW17081
AAW33698
AAW46615
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AAW33699
AAW10637
ABU07845
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AAR55059
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AAW19249
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AAW44323
ABU07841
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       Aaw31544 Human cyt
Aaw33699 AL-2-shor
Aaw10637 NIERKZ 1i
Abu07845 Human eph
Adq21436 Human sof
Ady51247 Human eph
Aaw17081 EPH famil
Aaw33698 AL-2-long
Aaw46615 Human tra
Abu07846 Mouse eph
Ady71239 Mouse eph
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Aaw19249 Human elk
Aaw36055 Human elk
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Mouse eph
Mouse eph
Human elk
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629.5	•	629.5	629.5	629.5	629.5	629.5	629.5	629.5	629.5	•	629.5	629.5	629.5	630.5	631	632	632	632	632	632
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Ady51246 Human eph	Adv73221 Human col	Adr82653 Human Eph	Adr86706 Human Eph	Adr67298 Human bla	Adp26886 Human Eph	Adn03886 Antipsori	Add89059 TAT245. 1	Abu07886 Novel hum	Aaw11308 Receptor-	Aaw06337 Full leng	Aar89287 Human LER	Aar92743 Human hep	Aar94655 Ligand fo	Aaw00288 Chicken E	Aar82606 Eph trans	Ady51245 Human eph	Adv97175 Human eph	Adr73462 Human eph	Ado28631 Human Epr	Adh76244 Human nov

Homo sapiens therapy. Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand; neurodegenerative disease; wound healing; neovascularisation; diagnosis; Human cytokine Lerk-8. 14-APR-1998 AAW31544; AAW31544 standard; protein; 340 (first entry) ₿

ALIGNMENTS

Location/Qualifiers

RRSULT 1
AAW31544
ID AAW3154
AC AAW3
XX AAW3
AC AAW3
AC AAW3
AC Homo
CONT 114-A
DE Homo
CONT HOM Key Peptide WPI; 1997-503043/46. N-PSDB; AAT89519. Misc-difference 19-MAR-1997; 09-OCT-1997 W09736919-A2 Cerretti DP; 21-MAR-1996; Domain Modified-site Domain Protein (IMMV) IMMUNEX CORP. 96US-00621146 97WO-US004533 /note= "N-glycosylated"
225. .251 28. .340 /label= Mat_protein 28. .224 210. .212 /note= "transmembrane domain" 252. .340 note= "residue 325 is Leu in Lerk-8 variant" note= 'note= "extracellular domain" label= Sig_peptide .340 "cytoplasmic domain"

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RESULT 2
AAW33699
ID AAW3
XX AAW3
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                    AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour; rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia; psoriasis; Alzheimer's disease; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1998
                                Peptide
                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                     AL-2-short
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                        (AL-28)
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1. .26
/note= "signal peptide"
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This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Epul-Acceptant is a AL-2-short (AL-2s) protein. The AL-2 is a novel Epul-Acceptant in the AL-2 is a novel Epul-Acceptant in the control of the AL-2 is a novel Epul-Acceptant in the AL-2 is a novel Epul-
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CC ischemia, infection, metabolic disease, nutritional deficiency, complete the survival or growth of complete the survival or growth as complete the survival or gravalysis. AL-2 cam be used to treat human neurodegenerative disorders, such as complete the survival or gravalysis. AL-2 can be used to treat human neurodegenerative disorders, such as complete the such as multiple sclerosis, Huntingtons chorea, Down's syndrome, compared the sused as cognitive enhancer, to enhance learning particularly complete they can promote axonal outgrowth and synaptic plasticity, particularly of hippocampal neurons that express AL-2 binding Eph-family receptors and cortical neurons that express AL-2 can also be used for wound healing, i.e. accelerating newvascularisation of, e.g. burns and ulcers. The encoding nucleic acids care useful in preparing antibodies that specifically bind to the AL-2 candulating various neuronal disorders. AL-2 antagonists can be used for mounts, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML), myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular Query Match Best Local Sequence 340 psoriasis B and rheumatoid arthritis 100.0%; Score 1850; DB 2; Pred. No. 2.5e-142; ; Mismatches 0; Length 340; patients stroke, in

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VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL

240 180 180 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYMNSANKRFQAEGGYVLYPQIGDRLDL MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL

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27-NOV-1995;
22-DEC-1995;
05-FEB-1996;
A novel human ligand for eph-related kinase (LERK) is designated NLERK2 (AAW10637). It is encoded by a cDNA clone (AAF60966) obtd. from a human foetal brain cDNA library. The novel receptor ligand can be expressed in transformed host cells and used in methods for regulating the development, maintenance or regeneration of different cells (e.g. neurons) and tissues in vivo and in vitro. Soluble NLERKZ peptides can be used to treat injury, disease or abnormality in the nervous system, and membrane-bound NLERKZ to modulate proliferation, different or survival e.g. in grafting procedures or transplantation. NLERKZ can also be used to raise antibodies for use in immunotherapy, and to detect anti-NLERKZ antibodies that may occur in some autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid mol. encoding ligand for eph-related kinase - useful for treatment of, pref. neuronal, cells to increase survival, proliferation and differentiation.
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                                                                                                                                                                                                                                                                                                                                                     16; Page 37-39; 71pp; English
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Best Local Simi
Matches 340;
                                                                                                 Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy; ligand-receptor binding modulator; ephrin ligand; angiogenesis; laberrant Ephrin-Tie biology; cell growth disorder; cell migration disorder; cell proliferation disorder; neovascularisation; ischaemia; infarction; tissue graft; transplant; human; ephrin-B3; tie receptor tyrosine kinase; Eph receptor ligand.
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                                                                                                                                                                                                                                                                                           Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002; 2002WO-IB002524.
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                                                                                                                                                                                                                                                                                           Kubo H;
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Pred. No. 2.
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Disclosure;

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modulator.

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The invention describes a method of identifying a modulator of binding CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method CC composition in the presence and in the absence of a putative modulator CC compound, and detecting the binding between Tie receptor and the Ephrin CC in the presence and in the absence of the putative modulator in the presence and in the absence of the putative modulator. The method is useful for identifying a modulator of binding between a Tie receptor CC tyrosine kinase and an Ephrin ligand. Modulators identified from the CC method are useful in modulating angiogenic processes, including CC lymphangiogenesis, for treating diseases associated with abserrant Ephrin-CC Tie biology, abserrant growth, migration or proliferation of cells that CC express a Tie receptor, or for promoting growth of vessel or covascularisation (e.g. ischaemic tissue, an infarction, a new or CC chronic compound, or a tissue graft or transplant). This is the amino CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of CC ligands that are bound to the membrane via a transmembrane domain and CC short cytoplasmic tail and function as Eph receptor ligands
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                                                                                                                                                            10-JUN-2004.
                                                                                                                                                                                                                                                                                             soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                       Human soft
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Early detection of soft tissue sarcoma comprises determining expressio of a gene in a first soft tissue sample and a normal soft tissue sampl and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                           expression
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor. Sequence 340 AA;

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                GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                    GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
                                                                                                                       VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                            SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
                                                                                                                                                                                                                                LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                                                                                                                                                     MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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                                                                                                                                                                                                                                                                                                                                    Score 1850; DB 8;
Pred. No. 2.5e-142;
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ADY51247 standard; protein;
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ADY51247;

19-MAY-2005 (first entry

ephrin-B3 SEQ Ħ NO:16.

ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic; antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatolog coagulant; immunostimulant; cerebroprotective; vasotropic; antiulc Homo sapiens. coagulant; immunostimulant; dermatological; ic; antiulcer.

US2005049194-A1

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RESULT 7
AAW17081
ID AAW1
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Best Local Similarity
Matches 340; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel use of ephrin, ephrin inhibitors, and ephrin receptors for alleviating a symptom of a disorder having reduced levels of hematopoiesis, having increased levels of cellular proliferation in an intestinal tract, or having an abnormal level of cellular proliferation in a tissue. A composition of the invention has cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal gen., dermatological, coagulant, immunostimulant, cerebroprotective, vasotropic, and antiulcer activity. The present sequence represents murine ephrin-B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of ephrin and its molecules for alleviating a symptom or a disorder with reduced levels of hematopoissis, increased levels of cellular proliferation in an intestinal tract, or abnormal level of cellular proliferation in a tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 340 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2001; 2001US-0345206P
02-UTU-2002; 2002US-0393272P
08-NOV-2002; 2002US-00291290
03-APR-2003; 2003US-0460488P
                09-AUG-1997
                                            AAW17081;
                                                                      AAW17081 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 16; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frisen J, Holmberg
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HOLMBERG
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Query Match
Best Local Similarity
Matches 339; Conserv
                                                                                                                                                                                                                                                                                                                                                          A novel ligand (AAW17081), designated Ef1-6 (or Eph transmembrane tyrosine kinase family ligand 6), binds to the Elk, Nuk/CeK5, HeK2/Sek4, tyrosine kinase family ligand 6), binds to the Elk, Nuk/CeK5, HeK2/Sek4, Htk and Sekl receptors on cells. Its amino acid sequence was deduced from a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6, truncated soluble polypeptides comprising the extracellular domain of Elf-6, and Ef1-6 ligandbodies comprising soluble Ef1-6 and the Fc portion of IgG can be expressed in host cells. These can be used to support neuronal and other Eph receptor-bearing cell populations for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding Ef1-6 ligand protein - used for promoting growth and proliferation of neuronal cells and in drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                         Sequence 340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-259021/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davie S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                               neurological disorders, in drug screening and to raise diagnostic
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           241
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                                                                                                                                            MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 1; 36pp; English.
GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
                                                    VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                     VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
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                                                                                                                                                                                                                                                      Conservative
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/label= Transmembrane_domain
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225. .249
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                                                                                                                                                                                                                                                                 99.7%;
99.7%;
                                                                                                                                                                                                                                                                  Score 1844; DB 2;
Pred. No. 7.8e-142;
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GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG

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301 301

GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV

340

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This is a AL-2-long (AL-21) protein. The AL-2 is a novel Eph-related CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in CC whom the nervous system has been damaged by trauma, surgery, stroke, CC ischaemia, infection, metabolic disease, nutritional deficiency, crowing system has been damaged by trauma, surgery, stroke, CC malignancy, or toxic agents, to promote the survival or growth of coneurons. They can be used to treat motoneuron disorders such as CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and CC various conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disorders, such as CC can be used as multiple sclerosis, Huntingtons chorea, Down's syndrome, CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome, CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome, CC in dementias or trauma, since they can promote axonal outgrowth and CC synaptic plasticity, particularly of hippocampal neurons that express AL-2 binding Eph-family receptors and cortical neurons that express AL-2. AL can also be used for wound healing, i.e. accelerating necleic acids are useful in preparing antibodies that specifically bind to the AL-2 protein. The antibodies and the AL-2 antagonists are useful in diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                Human AL-2 neurotrophic factor and related DNA - used to develop products for, e.g. treating neurologic disorders, angiogenesis disorders, tumours or rheumatoid arthritis or for wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL-21; AL-2; AL-2-long; human; treatment; neurological disorder; tumour; rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia; psoriasis; Alzheimer's disease; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-1997
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27. .455
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220. .245
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05-JUL-1996;

TNDOM (NOUNT

SINAI HOSPITAL CORP 96US-0021272P.

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AAW46615
AAW46615
AAW46615
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XX Elk
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Best Local Simi
Matches 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; signal transduction; axonogenesis; nerve cell; neurone; Alzheimer's disease; Parkinson's disease; Huntingdon's disease; demyelination; multiple sclerosis; amyotrophic lateral sclerosis; nervous system infection; Wernicke's disease; trauma; ischaemia; nutritional polyneuropathy; progressive supranuclear palsy; shy Drager's syndrome; multistem degeneration; olivo ponto cerebellar atrophy, peripheral nerve damage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human transmembrane ligand Elk-L3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elk-related receptor tyrosine kinase; transmembrane ligand;
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Pred. No. 1.9e-141;
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Matches 338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating transmembrane ligand for an Elk-related x kinase - by formation of a complex between an oligon receptor tyrosine kinase and a transmembrane ligand.
  ABU07846
                                     ABU07846 standard; protein;
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                                                                                                                                                                        GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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                                         340 AA
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Pred. No. 3.5e-141;
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                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of a putative
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                                                                                                                                                                                                                                                                                                          Sequence 340 AA;
                                                                                                                                                                                                                                                                                                                                           short cytoplasmic tail and function as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 121-122; 199pp; English.
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                                                                                                                                                                   MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                            SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
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95.6%;
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Pred. No. 1.3e
7; Mismatches
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Matches 325
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel use of ephrin, ephrin inhibitors, and ephrin receptors for alleviating a symptom of a disorder having reduced levels of hematopolesis, having increased levels of cellular proliferation in an intestinal tract, or having an abnormal level of cellular proliferation in a tissue. A composition of the invention has
                                                                                                                                                                                                                                                                                                cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal -gen., dermatological, coagulant, immunostimulant, cerebroprotective, vasotropic, and antiulcer activity. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of ephrin and its molecules for alleviating a symptom or a disorder with reduced levels of hematopoissis, increased levels of cellular proliferation in an intestinal tract, or abnormal level of cellular proliferation in a tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2001; 2001US-0345206P
02-JUL-2002; 2002US-0393272P
08-NOV-2002; 2002US-00291290
03-APR-2003; 2003US-0460488P
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                                                                                                                                                                                                                   Sequence
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MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                            MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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nilarity 95.6%;
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                                                                                                      Score 1780; DB 9;
Pred. No. 1.3e-136;
7; Mismatches 8;
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Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
myoclonic epilepsy ragged red fibre syndrome; anticonvulsant; antiarthritic;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                           comprises detecting
                                                                                                                                                                                                                                                                                    Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
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17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
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for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
   WPI; 1996-433391/43
                                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                                                                                                                   gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                 Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction; organogenesis; oncogenesis; tumour; neurological disorder; diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Eph receptor ligand ELF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW00287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW00287 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 285 AA;
                              Flanagan JG,
                                                                                           27-FEB-1995;
                                                                                                                      23-FEB-1996;
                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-1997
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                                                            HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                              Bergemann AD;
                                                                                           95US-00395415
                                                                                                                        96WO-US002673
                                                                                                                                                                                                                           31. .155
/label= Receptor_binding_site
                                                                                                                                                                                                                                                                         /label= Extracellular_domain
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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                                                                                                                                                                                                              Transmembrane_domain
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Murine hepatoma transmembrane kinase receptor ligand

Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;

neurodegenerative disease.

21-MAY-1996

(first

entry)

AAR92742; AAR92742

standard;

protein;

20-JUL-1994; 14-JUL-1995; 01-FEB-1996 WO9602645-A2

94US-00277722 95WO-US008812

(GETH) GENENTECH INC

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Best Local Simi
Matches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Eph receptor ligand ELF-2 (AAW00287) is strongly expressed in the anterior hindbrain and newly-forming somites of embryos at the early organogenesis stage of development. It is important in cellular communication during pattern formation. Its amino acid sequence was deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain cDNA library. The ELF-2 ligand can be used to alter neurological development, oncogenesis and growth regulation, to modulate binding of ELF-2 to the Eph receptor, and in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eph receptor ligand, ELF-2, and DNA encoding it is used prevent neurological diseases, and to modulate binding receptor, e.g. to prevent or treat tumour formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Fig 1A-B; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKPTIKFQEFSPNLWGLEFQKNK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                                                              YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                            WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
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                                                                                                                                                                                                                                                                                                                                                              YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 637.5; DB 2;
Pred. No. 1.8e-43;
19; Mismatches 129;
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ELF-2
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ADY51238
ID ADY51238
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XX ADY51
XX ADY51
XX IP-MP
DT 19-MP
DX MOUSE
XX Ephri
KW Ephri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and CC activate, the Htk receptor, have been identified in a variety of tissues CC using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the CC murine Htk ligand protein following a signal peptide cleavage is 34 kD CC with an estimated pl of 8.9. The murine and human ligands show 96% CC homology at the amino acid level. The DNA is used to produce recombinant CC ligands; for tissue- specific typing (partic. as a marker for breast CC cancer) and as a marker for human chromosome 13. The ligands (partic. in CC soluble form) are used to activate the tyrosine kinase domain of the Htk CR receptor, i.e. to stimulate or inhibit growth, differentiation, and/or CC activation of cells contg. the receptor, e.g. treatment of neurodegenerative diseases, since they are strongly expressed in the CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are CC also useful as a control or standard in assays, for generation of cantibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor costive cells, as research agent, in screening, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 139
                ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic; antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatolog coagulant; immunostimulant; cerebroprotective; vasotropic; antiulc
                                                                                                                         19-MAY-2005
                                                                                                                                                                                          ADY51238 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 336 AA;
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                                                                                      ephrin-B2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
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                                                                                                                                                                                                                                                                                 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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Pred.
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No. 1.8
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1.8e-43;
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                                    dermatological;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel use of ephrin, ephrin inhibitors, and ephrin receptors for alleviating a symptom of a disorder having reduced levels of hematopoiesis, having increased levels of cellular proliferation in an intestinal tract, or having an abnormal level of cellular proliferation in a tissue. A composition of the invention has cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal egen, dermatological, coagulant, immunostimulant, cerebroprotective, vascropic, and antiulcer activity. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of ephrin and its molecules for alleviating a symptom or a disorder with reduced levels of hematopoiesis, increased levels of cellular proliferation in an intestinal tract, or abnormal level of cellular proliferation in a tissue.
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02-JUL-2002; 2002US-039327P.
08-NOV-2002; 2002US-00291290.
03-APR-2003; 2003US-0460488P.
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307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ephrin-B2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRISEN J.
                                                                                                                                                                                                 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                            GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                             PNYEFYKLYLVGGAQGRRCEAPPAPNLLLICDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                          GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                       GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                            YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                         KYRRHRKHSPOHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR
                                                                                       WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                     GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
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GHPVYIVQEMPPQSPANIYYKV
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42.1%; Pred. No. 1.8
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L.8e-43;
hes 129;
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                                                             TADSVFC
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73

completed:

December

21,

14:30:19

306 310

Job time : 114.761 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1850
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PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          December 21,
                                                                                                                                                                                                                                                                                                                                                                MGPPHSGPGGVRVGALLLLG.....PVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2005, 14:22:09 ; Search time 20.956 Seconds
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1561.068 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARI

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	6	7	0	ហ	4	ω	N	,	Result No.
144.5	145	145	145.5	146	146.5	146.5	146.5	148	148.5	149	149	151.5	153.5	154.5	159	166	67.	169.5	•	•	176	179	•	•	613.5	•	632	637.5	Score
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438	931	674	305	675	1774	1492	1315	921	316	569	325	301	1670	1049	680	205	228	201	228	213	209	238	237	345	345	333	346	336	Length I
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collagen alpha cha	alpha	alpha	н	alpha 3	collagen alpha 1(X	alpha 1	alpha	alpha 1	ical pr	collagen - silkwor	ica	collagen 2 - Caeno	collagen alpha 3(I	alpha 1(collagen alpha 1(X		LERK-7 precursor -	uman	repulsive axon gui	- hu	ELF-1 protein prec		hypothetical prote		Stra1/Eplg2 protei	hepatoma transmemb	elk ligand - human	hepatoma transmemb	Description

ALIGNMENTS

RESULT 1 I49766

QY 311 YEKVSGDYGHP Db 307 YEKVSGDYGHP	Oy 251 WRRRAKPSES:	Oy 191 GAAHSLEPGKE : : : Db 194 GRSSTTSFFVK	Qy 134 DYYIIATSDGT : : : Db 134 DYYIISTSNGS	OY 74 PNYEFYKLYLV : : : Db 74 GQYEYYKVYNV	Qy 14 GALLLLGVLGU :: :: Db 17 GLLMVLCRTAI	Query Match Best Local Similarity 42.1 Matches 139; Conservative	A;Molecule type: mRNA A;Residues: 1-336 <res> A;Cross-references: UNIPR C;Genetics: A;Gene: HTK</res>
YEKVSGDYGHÞVYIVQDGÞÞQSÞÞNIYYKV 340 	WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310	GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER-DR 190	PNYEFYKLYLVGGAQGRRCEAPPADNLLLTCDRPDLDLRFTIKFQEYSDNLWGHEFRSHH 133 : : :	14 GALLLLGVIGLVSGLSLEPVYMNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73	34.5%; Score 637.5; DB 2; Length 336; 42.1%; Pred. No. 1.3e-37; :ive 49; Mismatches 129; Indels 13; Gaps 5;	A;Molecule type: mRNA A;Residues: 1-336 <res> A;Residues: 1-36 <res> A;Cross-references: UNIPROT:P52800; UNIPARC:UPI0000020B55; GB:L38847; NID:g769677; PIDN:I C;Genetics: A;Gene: HTK</res></res>
							PIDN:1

RBSULT 2 946993 elk ligand - human elk ligand - human C;Species: Homo sapiens (man) C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

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<u>,</u>δ
                                                                                                                                                                                                                                                                                                              C;Accession: 184743

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995

A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-A;Reference number: 149766; MUID:95199254; PMID:7534404

A;Accession: 184743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.;
EMBO J. 13, 3757-3762, 1994
A;Title: Molecular characterization of a family of ligands
A;Reference number: S46993; MUID:94349923; PMID:8070404
A;Accession: S46993
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                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-333 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                hepatoma transmembrane kinase ligand - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change
                                                                                                                                                                           A;Map
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A; Residues: 1-346 <BEC>
A; Cross-references: UNI
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                                                                 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVFRKFV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS
       PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                      GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANIYYKV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LLLLGVAGAGGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGGVRVGALLLLGVLGLVSGL----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
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                                                                                                      34.0%; Score 629.5; DB 2;
40.9%; Pred. No. 4.5e-37;
tive 52; Mismatches 130;
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                                                                                                            Indels
                                                                                                                                          Length
                                                                                                                                                                                                                                               GB:L38734; NID:g769675;
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                                                                                                                                           333;
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Stral/Eplg2 protein - mouse
C;Species: Mus muscullus (house mouse)
C;Species: Mus muscullus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 07-Jul-1996 #sequence_revision 07-Jul-1996 #text_change 09-Jul-2004
C;Date: 07-Jul-1996 #sequence_revision 07-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149780; A55507; A55062; S52670
C;Accession: 149780; Muid-2004; Mid-1996 #text_change 09-Jul-2004
C;Accession: 170, A5780; Mid-2004; Mid-1996 #text_change 09-Jul-2004
C;Accession: 149780; A559062; Mid-1996 #text_change 09-Jul-2004
C;Accession: 149780; Mid-1996 #text_change 09-Jul-2004
C;Acces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-89,'T',91-345 <SHA>
A;Cross-references: UNIPARC:UPI000016CADF;
C;Genetics:
A;Gene: EPIG2
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Genomics 24, 127-132, 1994
A;Title: Genomic organization and chromosomal localization
A;Title: Genomic organization and chromosomal localization
A;Title: Genomic ASS507; MUID:95203867; PMID:7896266
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R;Shao, H.; Lou, L.; Pandey, A.; Pasquale,
J. Biol. Chem. 269, 26606-26609, 1994
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A; Residues: 1-345 <FLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; not compared with conceptual translation
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Best Local S
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193
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                                                                                                                                                                                                                                                      SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH
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                                                                HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188
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Pred. No. 6.3e-36;
1; Mismatches 107;
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E.B.; Dix:
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A;Title: IERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionar A;Reference number: I58406; MUID:95022634; PMID:7936648
A;Accession: I58406
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hypothetical protein C43F9.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T19914
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPNYMGLEFKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS
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                                                                                                                                                                                                       KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK
                                                                                                                                                                                                                                                                        VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSLSTLASP
                                                                                                                                                                                                                                                                                                                                            VKT-----ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSK 236
                                                                                                                                                                                                                                                                                                                                                                             AHSLEPGKENLPGDPTSNATSRGAEGP------LPPPSMPAVAGAAGG------LA 236
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               #sequence_revision 15-Oct-1999 #text_change
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38.0%; Pred. No. 1.4e-35;
tive 52; Mismatches 107;
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C;Accession: I38849
R;KOZlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:438336; OMIM:601381
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Mortimore, B.
submitted to the EMBL Data Library
A;Reference number: Z19195
A;Accession: T19914
A;Status: preliminary; translated
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
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A;Map position: 4
A;Introns: 32/2; 96/
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A;Cross-references: UNIPROT:09U3M2; UNIPARC:UPI0000078016; EMBL:Z82262; PIDN:CAB54195.1;
A;Experimental source: clone C43F9
C;Genetics:
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A; Residues: 1-238 < RES>
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Best Local S
Matches 65
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Best Local 9
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 RKPVSEMP---
                                     QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
                                                                          QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP
                                                                                                             SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF
                                                                                                                                                                                                                          GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTDHVISVHIGDRVSIRCPKSDET
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                                                                                                                                                                                                                                                               9.7%;
ilarity 28.4%;
Conservative 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                               Score 179; DB 2;
Pred. No. 1.3e-05;
14; Mismatches 80
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   -MERDRGAAHSLE----
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                                                                                                                                                                                                                                                                 80;
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                                                                                                                                                                                                                                                                                                  Length 238;
   -- PGKENLP 204
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K;SnBO, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
J. Biol. Chem. 270, 3467-3470, 1995
A;Title: CDNA cloning and characterization of a Cek7 receptor protein-tyrosine A;Reference number: A55873; MUID:95181289; PMID:7876076
A;Accession: A55873
                                                                                                                                                          C;Accession: JE0322
R;Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T. Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, chromosal mapping, and tissue expression of the A;Reference number: JE0322; MUID:99045414; PMID:9826538
A;Accession: JE0322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change C;Accession: A54984; A55873 R;Cheng, H.J.; Flanagan, J.G.
                                                                     A;Cross-references: UNIPROT:O43921; C;Superfamily: axon guidance signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P52801; UNIPARC:UPI0000020CE3; GB:U14941; NID:g558836; R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
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A; Residues: 1-209 < CH
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A; Title: Identification and cloning of ELF-1, a developmentally A; Reference number: A54984; MUID:95007776; PMID:7522971
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A; Residues: 1-213 < AAS>
                                                                                                                                           A; Status: preliminary
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A; Residues: 1-209 < SHA>
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Best Local S
Matches 58
                                                                                                                                                                                                                                                                     ;Species: Homo sapiens (man);Date: 05-Feb-1999 #text_change;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Mus musculus (house mouse)
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 Matches
                                   Query Match
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 43;
                  Similarity
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36.8%;
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Pred. No. 1.8e-05
                  Score 175.5; DB Pred. No. 2e-05;
Pred. No. 2e-(
); Mismatches
                                                                       UNIPARC:UPI000016A442; protein
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                                   BB
 51;
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 Indels
                                 Length
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                                                                                          GB:AJ007292; NID:g3688367;
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C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Recession: I38850
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 82, 359-370, 1995
A;Title: In vitro guidance of retinal ganglion cell axons
A:Reference number: A57084; MUID:95360980; PMID:7634326
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-228 <DRE>
                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P52804; UNIPARC:UPI0000129C92; GB:X90377; NID:g1061113; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A57084; A; Accession: A57084
                     A;Gene: GDB:EPLG4
A;Cross-references: GDB:438337;
                                                                   A; Cross-references:
C; Genetics:
                                                                                                                A; Molecule type: mRNA
A; Residues: 1-201 < RES>
                                                                                                                                                                                                                                                                                                                                                                          LERK-4 - human
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYWNSANKRFQA----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPN------GPLK
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1q21-1q22
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                                                                                           UNIPROT: P52798; UNIPARC: UPI0000129C90; EMBL: U14188; NID: g642834; PID
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28.9%; Pred. No. 4.
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                          OMIM:601380
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thes 91;
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Neuron 14, 973-981, 1995
A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine A;Reference number: I58170; MUID:95267434; PMID:7748564
A;Accession: I58170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P52803; UNIPARC:UPI0000129C93; GB:S77167; NID:g914184; R;KOZ10sKy, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K. submitted to the EMBL Data Library, May 1995
A;Reference number: G08477
A;Accession: G01812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <RES>
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A;Molecule type: mRNA
A;Residues: 1-228 <KOZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: AL-1
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                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GDB:568757; OMIM:601535
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Best Local
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                                                                                                                                         91 DHTSKGFKRWECNRPHSPN------GPLKFSEKFQLFTFFSLGFEFRPGREYFYISS 141
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                                                                                                       S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                                                                                                                                                                                                                  VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG------
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                                  PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
                                                                                                                                                                                                             VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
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 PADDTV---HESAEPSRG-ENAAQTPRIPSRL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                    -CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE
                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                              Score 167.5; DB 2
Pred. No. 7.9e-05;
9; Mismatches 81
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                                                                                                                                                                                                                                                                                  81;
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S31216
                  A;Reference number: S30127;
A;Accession: S30127
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A; Residues: 1-680 < K
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A36377
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                                                                                                                                                                                                                                                                                                                    A;Accession: S28807
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A; Residues: 1-205 < HOL>
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preliminary
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A;Cross reconstruction A;Cross reconstruction B.R.
R;Appte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type
A;Title: Characterization of the mouse type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 1(X) chain precursor - mouse ()Species: Mus musculus (house mouse) ()Species: Mus musculus (house mouse) (C;Date 30.0-sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: S31216; S28807; $\overline{S22215}; S30127; 148299; S26\overline{S31830} R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M. RyKong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M. Stur. J. Biochem. 213, 99-111, 1993
A;Title: Intron-exon structure, alternative use of promoter and expression of the A;Reference number: S31216; MUID:93238750; PMID:8477738
                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-285,'A,'287-680 <ELI>
A;Residues: 1-285,'A,'287-680 <ELI>
A;Residues: 1-285,'A,'287-680 <ELI>
A;Cross-references: UNIPARC:UPI0000026913; EMBL:X67348; NID:g50480; PIDN:CAA47763.
A;Zilima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.;
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collag A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B61 protein precursor - human (Agn) (Species: Homo sapiens (Man) (C;Species: Homo sapiens (Man) (C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004 (C;Accession: A36377 R;Holzman, L.B.; Marks, R.M.; Dixit, V.M. Mol. Cell. Biol. 10, 5830-5838, 1990 Mol. Cell. Biol. 10, 5830-5838, 1990 A;Title: A novel immediate-early response gene of endothelium is induced by A;Reference number: A36377; MUID:91042512; PMID:2233719 A;Accession: A36377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:005306; UNIPARC:UPI000016CBAA; EMBL:Z21610; NID:g49793; PIDN R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Crostiochem. J. 289, 247-253, 1993
                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 385-450, 'K', 452-627 <ELA>
A; Cross-references: UNIPARC: UPI000016CBAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and A;Reference number: S28807; MUID:93143676; PMID:8424763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P20827; UNIPARC:UPI0000129C89; GB:M57730; GB:M37476; NID:g179
C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.0%; Score 166; DB 2; I
27.5%; Pred. No. 8.9e-05;
ative 31; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLRLKVTVSGKITHSPQAHVNPQE
                                                                                                                                                                                    EMBL: X63013; NID: g49795; PIDN: CAA44741.1;
                         y Collagen gene
PMID:8492743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 205;
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A;Introns: 51/3
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F;1-18/Domain: sdgnal sequence #status predicted <SIG>
F;1-18/Domain: sdgnal sequence #status predicted <MAT>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004
C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehr Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino A;Reference number: A02862; MUID:80026026; PMID:488906
A;A;Accession: A02862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPARC:UPI00001773E6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen A;Reference number: S26397; MUID:88087150; PMID:2 A;Accession: S26397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R. Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen A;Reference number: I48299; MUID:92267014; PMID:1587271
A;Accession: I48299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 'SDGYFSQ', 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',56
A;Cross-references: UNIPARC:UDI000016CCAC; EMBL:X65121; NID:g50482; PIDN:CAA46237.1;
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A;Cross-references: UNIPARC:UPI00001773E5
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                                                                                                                                                                                                                             collagen alpha 1(III) chain - bovine
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Best Local S
Matches 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGPPHSGPGGV-RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLD
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Pred. No. 0.001;
0; Mismatches 108; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVY 323
                                                                                                                                                                                                                                                                                                                                                             492
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A;Cross-references: UNIPARC:UPI0000173B8B
R;Bentz, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type II
A;Reference number: A38002; MUID:80026028; PMID:4888
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
A;Residues: 87-106;1017-1029;1037-1049 <HENDERC:UPI0000173B91; UNIPARC:UPI0000173B92
A;Cross-references: UNIPARC:UPI0000173B90; UNIPARC:UPI0000173B91; UNIPARC:UPI0000173B92
C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are h;
C;Comment: The type III collagen molecule is a trimer of identical chains, linked to each
C;Comment: The type III collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: collagen alpha 1(III) chain #status experimental <CAB>
F;1-104/Region: amino-terminal nonhelical telopeptide
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A;Molecule type: protein
A;Residues: 423-571 < ABN>
A;Cross-references: UNIPARC: UPI0000173B8C
A;Cross-references: UNIPARC: UPI0000173B8C
A;Cross-references: UNIPARC: UPI0000173B8C
A;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
A;Title: The covalent structure of calf skin type III collagen.
A;Title: The covalent structure of calf skin type III collagen.
                                                                                                                     F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #sf F;107,950/Modified site: allysine (Lys) #status predicted F;107/Binding site: carbohydrate (Lys) (covalent) #status ex F;1040,1041/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                       F;15-1040/Region: helical
F;587-589/Region: cell attachment
F;752-754/Region: cell attachment
F;875-877/Region: cell attachment
F;878-880/Region: cell attachment
F;935-937/Region: cell attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Cross-link analysis of the C-telopeptide domain A;Reference number: S71946; MUID:96404897; PMID:8809038 A;Accession: S71946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Dewes, H.; Fietzek, P.P.; Kuehn,
Hoppe-Seyler's Z. Physiol. Chem. 36
A;Title: The covalent structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 572-808 <LAN>
A;Cross-references: UNIPARC:UPI0000173B8D
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Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832,
A;Title: The covalent structure of calf skin t
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A; Residues: 1-242 < FIE>
A; Cross-references: UNIPROT: P04258; UNIPARC: UPI0000173B8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: skin R; Henkel, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979 A;Title: The covalent structure of calf skin type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A38003; A; Accession: A38003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UPI0000173B8F
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A;Residues: 809-947 <DEW2>
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MUID:80026030; PMID:488910
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                                                                                                                                                                                                                           GO; GO:0005687; C:integral to plasma membrane; TAS. GO; GO:0005005; F:transmembrane-ephrin receptor act; GO; GO:0007267; P:cell-cell signaling; TAS. GO; GO:0007399; P:neurogenesis; TAS. InterPro; IPR001799; Ephrin.
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MEDLINE=99211388; P
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SUBUNIT: Interacts with GRIP1 and GRIP2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Highly expressed in brain; expressed embryonic floor plate, roof plate and hindbrain segments.
SIMILARITY: Belongs to the ephrin family.
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U66406; AAC51203.1; -; mRNA.
U62775; AAC50707.1; -; mRNA.
BC022499; AAH22499.1; -; mRNA.
BC042944; AAH42944.1; -; mRNA.
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Z., Henzel W.J.;
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WEDLINE-2238257; Pubmed-12477932; DOI=10.1073/pnas.242603899;

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& Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

& Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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PRINTS; PR01347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Differentiation;
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0007628; P:adult walking behavior; I
GO; GO:0007628; P:axon choice point recogni
InterPro; IRR001799; Ephrin.
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Development 127:1397-1410(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitro. May play a role in constraining the orientation of longitudinally projecting axons.
SUBUNIT: Interacts with GRIP1 and GRIP2 (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed on lateral floor plate cells, specifically on commissural axon segments that have passed throug the floor plate. Expressed in cells of the retinal ganglion cell layer during retinal axon guidance to the optic disk.
DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European
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BC052001; AAH52001.1; -; mRNA.
BC058617; AAH58617.1; -; mRNA.
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7; Mismatches
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Extracellular (Potential).

Potential:

Cytoplasmic (Potential).

PDZ recognition motif (Potential).

N-linked (GlcNAc...) (Potential).
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STRAIN=C57BL/6J; TISSUE-Head;
MEDLINE=2235463; PubMed=1246685; DOI=10.1038/nature01266;
MEDLINE=2235463; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354663; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354663; PubMed=12. Adachi J., Bono H., Kondo S.,
MEDLINE=22354663; PubMed=10.1038/nature01266;
MEDLINE=2235463; DOI=10.1038/nature01266;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Ephrin B3 (16 days embryo head cDNA, RIKEN full-length
library, clone:Cl30048B01 product:m-ephrin-B3).
Name=Efnb3; ORFNames=RP23-56120.5-001;
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MEDLLNE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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Submitted (FEB-2005)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                            ional annotation of a full-length mouse cDNA collection."; 409:685-690\,(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
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                                                  nyosawa H.,
Gojobori T
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RA Kanal A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magsshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Ol D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wanghaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Wasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Hara A., Hayashizaki Y.,
RA Hara Hayashizaki Y.,
RA Hara Hayashizaki Y.,
RA Hara Hayashizaki Y.,
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RA Hara Hayashizaki Y.,
RA Hayashizaki Y.,
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A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hitramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohaato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Submitted (JUL-2001) to the EMBL/Genjank/DDBJ databases.

R EMBL; AK048305; BAC332921; -; RRNA.
                                         Query Match
Best Local (
    Matches
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MEDLINE-20530913, PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.
Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
Chira M., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
Genome Res. 10:1757-1771(2000).
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                                              Similarity
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    Conservative
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7;
                                              Score 1780;
Pred. No. 1
                                                                                                                                                                                   52F3D58FD209A6B8
Mismatches
                                              .2e-106;
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                                                                                       Length 340;
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MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYMNSANKRFQAEGGYVLYPQIGDRLDL

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RESULT 4
Q90231 BARE
Q90231 BAC
Q90231;
DT 01-DEC-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; IEA.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODOM; PE000253; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
SECULENCE 331 AA; 35638 MW; 6A
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01-DEC-2001
01-OCT-2003
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Dev. Biol. 234:470-482(2001).
EMBL; AF375227; AAK64277.1; -; mRNA.
HSSP; P52800; 1IKO.
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MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281; Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B., Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.P. Thomas M.C., Cleary J.A., Thomas M.C., Thomas M.C., Cleary J.A., Thomas M.C., Cleary J.A., Thomas M.C., Cleary J.A., Thomas M.C., Cleary J.A., Thomas M.C., Thomas M.C., Thomas M.C., Cleary J.A., Thomas M.C., T
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Actinopterygii; Neopterygii;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENSDARG00000008177; Danio rerio
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                                                                                                                                                                                   PHSSPNYEFYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE
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                                                                                                                                                PRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
gii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 923; DB 2;
Pred. No. 1.5e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases EMBL; BC095605; AAH95605.1; -; mRNA. SEQUENCE 342 AA; 36885 MW; 1629532234F85386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Efnb3 protein.
Name=efnb3;
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                                                                                                                      PRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequences.";
l. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.9%; Score 923; DB 2;
54.8%; Pred. No. 1.6e-51;
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Last sequence update)
Last annotation update)
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() Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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Best Local :
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SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryonic head;

MEDLINE=20099673; PubMed=10633856;

DOI=10.1002/(SICI)1097-0177(199912)216:4/5<361::AID-DVDY5>3.0.CO;2-W;

Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,

Wilkinson D.G., Brandli A.W.;

Wilkinson D.G., Brandli A.W.;

"Comparative analysis of embryonic gene expression defines potential interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";

Dev. Dyn. 216:361-373(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ236866; CAB65511.1; -; mRNA.
HSSP; P52800; 1IKO.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR002086; Aldehyd_dehydrog
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ve.
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01347; EPHRIN.

PRODOM; PD002533; Ephrin; 1.

PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.

PROSITE; PS01299; EPHRIN; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ephrin-B3 precursor.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9PT69 XENLA
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                                                                                                       LPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESR
                                                                                                                                         TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVPNPDIPN
                                                                                                                                                                                                                                                                                              GGAQG-RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG
                                                                                                                                                                                                                                                                                                                                                                                                           VSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLV
:| |||:|:||||: ||||:
HPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPV
                                                                                                                                                                                              TREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSL-EPGKEN
                                                                                                                                                                                                                                                                       GTKEEMSSCSILRTPNLLLTCDRPSQDLRFTIKFQEFSPNLWGHEFQSQRDYYIIATSDG
                                                                                                                                                                                                                                                                                                                                                                             ISALSLDPIYWNSSNKRFEDTEGYVLYPQIGDRLDLLCPRSEPQGPFSSSPYEYYKLYLV
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35913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.7%; Score 919; DB 2; 60.4%; Pred. No. 2.7e-51;
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Last annotation update)
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ia; Pipoidea; Pipidae;
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                      RA Strausberg R.D., Felmpold E.A., Grouse L.H., Derged J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Blosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
10-MAY-2005 (Rel.
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10-MAY-2005 (Rel. 47, Last annotation update)
Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand
(LERK-5) (HTK ligand) (HTK-L) (ELF-2).
Name=Efnb2; Synonyme=Elf2, Epl5, Epl5, Htkl, Lerk5;
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Bennett B.D., Zeigler F.C., Gu Q.,
Gillett N., Matthews W.;
"Molecular cloning of a ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
Muroidea; Muridae; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95379837;
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                               full-length human
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"Crystal
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Development 127:1397-1410(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crystal structure of an Eph receptor-ephrin Nature 414:933-938(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170. PubMed=11703926; DOI=10.1016/S1534-5807(01)00002-8; Toth J., Cutforth T., Gelinas A.D., Bethoney K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20171264; PubMed=10704386; Imondi R., Wideman C., Kaprielian
                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor tyrosine kinase EPHB4.

I SUBCELULAR LOCATION: Type I membrane protein.

TISSUE SEBCIFICITY: Expressed on lateral floor plate cel specifically on commissural axon segments that have pass the floor plate. Expressed in cells of the retinal gangl layer during retinal axon guidance to the optic disk.

Layer during retinal axon guidance to the optic disk.

DEVELOPMENTAL STAGE: Expressed in the floor plate throug period of commissural axon pathfinding.

PMM: Inducible phosphorylation of tyrosine residues in t cytoplasmic domain (By similarity).
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Henkemeyer M., Nikolov D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
PubMed=11780069; DOI=10.1038/414933a;
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SUBUNIT: Interacts with PDZRN3 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                          European
                                                                                                                                                                                                                                                                                                                                                                                                                         Swiss-Prot entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on it
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MOTIF GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:000586; C:plasma membrane; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001945; P:lymph vessel development;
GO; GO:0009887; P:organogenesis; IMP.
InterPro; IPR001799; Ephrin. PDB; 11KO; X-ray; P=30-207.

PDB; 1KGY; X-ray; E/F/G/H=31-168

Ensembl; ENSMUSG00000001300; Mus SIGNAL Neurogenesis; PROSITE; PS01299; ProDom; PD002533; MGI:105097; Efnb2 149766; 149766 U16819; AAA99708.1; -; mRNA. L38847; AAC42052.1; -; mRNA. U30244; AAA82934.1; -; mRNA. BC057009; AAH57009.1; -; mRN PF00812; Ephrin; 1 S; PR01347; EPHRIN 29 233 254 334 Phosphorylation; P99; EPHRIN; 1.
Developmental Ephrin; 1. protein; -; mRNA Potential.
Cytoplasmic (Potential)
PDZ recognition motif (Extracellular (Potential). Potential Signal; musculus. Differentiation; Glycoprotein; (Potential)

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RESULT 8
Q4FOM3_MOUSE Q4FOM3;
AC Q4FOM3;
AC Q4FOM3;
DT 13-SEP-2005 (TrEMBLrel. 31,
DE Bfnb2 protein.
GN Name-Efnb2;
GN Name-Efnb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordat
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                                                                                                                                                                     GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
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                                                                                                                                                                                                                         GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                              YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                 KYRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                                                                                           GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFÄGIÄSGCIIFIVIIITLVVLLL
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                                                                                       YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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                                                                                                                                                                                                                                                                                           Chordata;
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Pred. No. 3.5e
19; Mismatches
                            Last sequence update)
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A -> T (
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N-linked
  Craniata; Vertebrata; Euteleostomi;
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Matches 139
                                                                                                                                                      MEDLINE-94349923; PubMed=8070404;
Beckmann M.P., Cerretti D.P., Baum P., Vanden Bos T Farrah T., Kozlosky C., Hollingsworth T., Shilling Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
"Molecular characterization of a family of ligands tyrosine kinase receptors.";
EMBO J. 13:3757-3762(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephrin-B1 precursor (EPH-related receptor tyrosine (LERK-2) (ELK ligand) (ELK-L).
Name=EFNB1; Synonyms=EFL-3, EPLG2, LERK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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SEQUENCE 336 AA; 37202 MW; D08894996E399554 CRC64;
MEDLINE-95063919; PubMed=7973638;
Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C.,
Pawson T., Goldfarb M., Yancopoulos G.D.;
"Ligands for EPH-related receptor tyrosine kinases tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Euarchontogi
Muroidea; Muridae; Murinae; Mus
MCBI_TaxID=10090;
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TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euarchontoglires; Primates; Cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.5%; Score 637.5; DB 2 42.1%; Pred. No. 3.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ند ه.,
                                                                                                                                                                                                                                                           Bos T., J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ata; Euteleostomi;
Catarrhini; Homir
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                                                          Lhotak
                                                                                                                                                                                                                                                                                         James
                                                                                                                                                                                                              eph-related
                                                                                                                                                                                                                                                                 Maraskovsky
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for activity.";

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RA RICHARGE S., SCOTTE G., STEFFEN D., SOGETYPEN E., Wheeler D.A.,
RA WORLEY K.C., Alnescough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,
RA Ashwell R.I., Babbage A.K., Baggyley C.L., Ballabio A., Banerjee R.,
RA Ashwell R.I., Babbage A.K., Baggyley C.L., Ballabio A., Banerjee R.,
RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
Clore C.M., Collec C.M., Colleg S.,
RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Colleg S.,
RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Colleg S.,
RA Ciccodicola A., Clark S.Y., Dunham A., Dunn M., Durbin K.J., Dutka M.J.,
RA Driger H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutka M.J.,
RA Driger J., Joseph S., David R., Dunham J., Doses S.L.,
RA Cades T., Ellwood M., Bmery-Cohen A., Errington H., Evans K.L.,
RA Fallkre T., Francis F., Frankland J., Fraser A.E., Galgoczy P.,
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA Griffiths C., Grocock R., Gu Y., Gallliam R., Hamilton C., Hart E.A.,
RA Harwes A., Heath P.D., Heitmann K., Henrig S., Herrandez J.J.,
RA Hawes A., Heath P.D., Heitmann K., Henrig S., Herrandez J.,
RA Hawes A., Heath P.D., Holf R., Gilver J., Holes J., Kerahaw J.K., Khan Z.,
RA Lord G. K., Luyd D. M., Loulseged H., Loweland J.E., Lovell J.D.,
RA Hunte B.J., Klages S., Knights A.J., Kosiura A., Metchew I.J., Liu W.,
RA Lord G. K., Luyd D. M., Loulseged H., Loweland J.E., Lovell J.D.,
RA Millen S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA Millen S., Miner G., Paracce A.V., Reichwald K., Rhodes S.,
RA Ridler K.A., 
                                                                                                                                                                                                                                                          Wilson R.K., Waterry
Wilson D.L., Weinstock G., burn
Nelson D.L., Beck S., Rogers J.,
Gibbs R.A., Beck S., Rogers J.,
Gibbs R.A., Beck S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fletcher F.A., Hubbner K., Shaffer L.G., Monaco A., Mueller U., Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J., Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.; "Assignment of the human Elk ligand gene, EPLG2, to chromosome regard?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSS M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A. Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak Jones M.C., Hurles M.E., Andrews T.D., Scott C.E., Searle S. Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E. Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L., Branche G., Goott G., Steffen P., Godgson R., Metzker M.L., Branche G., Goott G., Steffen P., Godgson R., Metzker M.L.,
                                                                                 TISSUE=Eye, and skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=15772651;
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                                                      MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ettachment or clustering 266:816-819(1994).
                                                                                                                                                              SEQUENCE [LARGE SCALE MRNA].
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Feingold
                                                      PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ
E.A.,
                                                                                                                                                                                                                                                                                                                      ×
Grouse L.H.,
                                                                                                                                                                                                                                                                                                                      chromosome.
                                                 DOI=10.1073/pnas.242603899;
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          Derge J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K., Muzny D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . s.,
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Blosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rodriguez A.C., Grimwood J., Schemutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                  VARIANTS CFNS ARG-27; LEU-54; SER-119; HIS-119; ALA-137; PHE-1 SER-151; SER-153; TYR-153 AND ARG-182.
PubMed=15959873; DOI=10.1002/humu.20193;
Wieland I., Reardon W., Jakubiczka S., Franco B., Kress W., Vincent-Delorme C., Thierry P., Edwards M., Koenig R., Rusu C. Schweiger S., Thompson E., Tinschert S., Stewart F., Wieacker "Twenty-six novel EFNBI mutations in familial and sporadic craniofrontonaeal syndrome (CFNS).";
Hum. Mutat. 26:1-6(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=15124102; DOI=10.1086/421532; Wieland I., Jakubiczka S., Muschke P., Gerlach K.L., Adams R.H., Wieacker P.; "Mutations of the ephrin-B1 gene cause Am. J. Hum. Genet. 74:1209-1215(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Twigg S.R.F., Kan R., Babbs C., Bochukova E.G., Robe wall S.A., Morriss-Kay G.M., Wilkie A.O.M.; Mutations of ephrin-B1 (EFNB1), a marker of tissue formation, cause craniofrontonasal syndrome."; Proc. Natl. Acad. Sci. U.S.A. 101:8652-8657(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "EphrinB ligands recruit membrane microdomains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=15340161, DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analyverified cleavage sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS CFNS THR-62; SER-98; PRO-115; HIS-11
VAL-151; PRO-155; ILE-158 AND VAL-158, AND VAP
PUBMed=15166289; DOI=10.1073/pnas.0519101;
PubMed=15166289; DOI=10.1073/pnas.0519101;
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MEDLINE=99211388; PubMed=10197531;
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                                                                                                   Binds to, and induce the collapse of, commissural axons/growth cones in vitro. May play a role in constraining the orientation longitudinally projecting axons (By similarity). SUBUNIT: Interacts with GRIP1 and GRIP2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal musc
                                            PTM:
  cytoplasmic
DISEASE: Def
                                                               INDUCTION: By TN
                                                                                                                                                                                                                                FUNCTION: Binds to the receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22:511-524(1999)
Inducible phosphorylation of tyrosine residues plasmic domain (By similarity).
ASE: Defects in EFNB1 are a cause of craniofront
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFNS LEU-54 AND ILE-111
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                                                               By TNF-alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; DOI=10.1016/S0896-6273(00)80706-0; Scheiffele P., Herb A., Seeburg P.H.
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AND VARIANT
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      craniofrontonasal
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Best Local
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                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ephrin-B2 precursor (EPH-related receptor tyrosine (LERK-5) (HTK ligan) (HTK-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U09304; AAA53093.1; -; mRNA.
EMBL; L37361, AAA52369.1; -; mRNA.
EMBL; U09303; AAB41127.1; -; mRNA.
EMBL; AL136092; CAB86409.1; -; Genomic_DNA.
EMBL; BC016649; AAH5649.1; -; mRNA.
EMBL; BC05279; AAH52979.1; -; mRNA.
EMBL; BC05279; AAH52979.1; -; mRNA.
                                     Name=EFNB2; Synonyms=EPLG5, HTKL, Homo sapiens (Human).
             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                      EFNB2 HUMAN
P52799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P52800; 1IKO.
Ensembl; ENSG00000090776; Homo
HGNC; HGNC:3226; EFNB1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                syndrome (CFNS) [MIM:304110]; also known as craniofrontonasal dysplasia (CFND). CFNS is an X-linked inherited syndrome characterized by hypertelorism, coronal synostosis with brachycephaly, downslanting palpebral fissures, clefting of the nasal tip, joint anomalies, longitudinally grooved fingernails a other digital anomalies.

SIMILARITY: Belongs to the ephrin family.
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                                                                                                                                                    STANDARD;
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EMBL; EMBL;

; U16797; ; L38734; ; U81262;

AAA99707. AAC41752. AAD03786.

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mRNA. mRNA. mRNA.

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and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

C. FUNCTION: Binds to the receptor tyrosine kinases EPH May play a role in constraining the orientation of 1 projecting axons (By similarity).

C. I SUBUNIT: Interacts with PDZRN3 (By similarity). Bind receptor tyrosine kinases EPHB4 and EPHA3.

C. I SUBCELLULAR LOCATION: Type I membrane protein.

I TISSUE SPECIFICITY: Lung and kidney.

C. I SUBCELLULAR LOCATION: Type I membrane protein.

I TISSUE SPECIFICITY: Lung and kidney.

C. I SIMILARITY: Belongs to the ephrin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full
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NUCLEOTIDE SEQUENCE.

WEBH J., Jung B., Kerbel R.

Wogt T., Stolz W., Welsh J., Jung B., Kerbel R.

Landthaler M., McClelland M.;

"Overexpression of Lerk-5/Eplg5 messenger RNA:

"Increased tumorigenicity and metastatic potenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bennett B.D., Zeigler F.C., Gu Q., Fend Gillett N., Matthews W.; Gillett N., Matthews W.; The moderate cloning of a ligand for the tyrosine kinase Htk.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jenkins N.Ā., Fletcher R.Ā.;
"Isolation of LERK-5: a ligand of
kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5; Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P., Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J., Jenkins N.A., Fletcher R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                               Swiss-Prot entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                 modified and this
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RESULT 11

QSJV56 HUMAN
QSJV56;

TO STOTE (TEMBLE) 30, Created)

DT 10-MAY-2005 (TEMBLE) 30, Last sequence
DT 10-MAY-2005 (TEMBLE) 30, Last sequence
DT 10-MAY-2005 (TEMBLE) 30, Last annotation

Exphrin-B2 (Fragment).

GN Name-EFNB2; ORFNames=RP11-272L14.1-001;
OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; V
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Best Local S
Matches 135
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CARBOHYD
DISULFID
DISULFID
SEQUENCE
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TOPO DOM
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EMBL;
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SIGNAL 1
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ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM, 600527; -.
GO:0005887; C:integral to plasma membrane;
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0046875; F:ephrin receptor binding; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0009653; P:morphogenesie; TAS.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSG00000125266;
HGNC; HGNC:3227: EFNED
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SMR; P52799; 27-167
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                                                                                                                                                                                                                                                                                              GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                    YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                                                                                                             WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                                                                     DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                                                          GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK
                                                                                                                                                                                                                                                                                                                                                                                         PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
                                                                                                                                                                                                                                                                                                                                                                                                                          GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                     KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                         GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36923 MW
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                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 629.5; Pred. No. 1.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
Cytoplasmic (Potential).
PDZ recognition motif (Potential).
N-linked (GlcNAc. . ) (Potential).
N-linked (GlcNAc. . ) (Potential).
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By similarity.
6D9932A632626AEA CRC64;
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Extracellular
   Craniata;
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mRNA
mRNA
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   Vertebrata; Euteleostomi;
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REPUILATION OF THE PROPERTY OF
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Matches
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                                                                                                                                                                                            Menzel P., Pasquale E.B.;
"Coding sequence of chicken epi
Submitted (AUG-1999) to the EMI
EMBL; AF180729; AAD53948.1; -;
HSSP; P52800; IIKO.
SMR; O9PUJ4 29-169
Ensembl; ENSGALG00000016856; Ga
GO; GO:0016020; C:membrane; IEA
                            CHAIN
                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephrin-B2 precursor.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata,
Archosauria, Aves, Neognathae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2005) to the EMBL/GenBank/DDBJ EMBL; AL138689; CAI39907.1; -; Genomic_DNA. GO; GO:0016020; C:membrane; IEA. NON TER 33 33 33 AA; 36923 MW; 6D9932A632626AE
        SEQUENCE
                                                                                                                                Pfam; PF00812; Ephrin; 1
PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PUJ4 CHICK PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                          PROSITE;
                                                                                                                                                                              InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                PD002533;
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                                                                                            PS01299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
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28
333
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        AA;
                                                                                            Ephrin;
EPHRIN;
        27 F
333 e
36761 MW;
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36923 MW; 6D9932A632626AEA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.0%; Score 629.5; DB 2
40.9%; Pred. No. 1.1e-32;
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Last
                                                                                                                                                                                                         IEA.
                                                                                                                                                                                                                                                                                                          ephrin-B2.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                      -; mRNA.
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        Potential.
ephrin-B2.
; 4C28E8CB211B7783
                                                                                                                                                                                                                           Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
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               CRC64;
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Best Local Similarity
Matches 135; Conser
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073612;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-May-2nd precursor (CEKS ligand) (CEL5-L).
                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
Probom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Differentiation;
Phosphorylation; Signal; Transmembrane.
                                                                                          EMBL; U72394; AAC07986.1;
HSSP; P52800; 1IKO.
                                                                                                                                                                                           Thie
                                                                                                                                                                                                                                                                                                                                                                                                                        Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                 nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHICK
                                                                                                                                                 Buropean
                                                                                                                                                                                                                                         SUBUNIT: Binds to the receptor tyrosine kin with GRIP1 and GRIP2 (By Similarity). With GRIP1 and GRIP2 (By Similarity) substitution in the SUBCELLULAR LOCATION: Type I membrane prote PTM: Inducible phosphorylation of tyrosine
                                                                                                                                                                                                                                                                                             early retina.";
. Biol. 182:256-269(1997).
                                                                                                                                                                                                                 cytoplasmic domain (By similarity).
SIMILARITY: Belongs to the ephrin family.
                                                                                                                                                Swiss-Prot entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation EUROpean Bioinformatics Institute. There are no restrictions on it song as its content is in no way modified and this statement is no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYYVISTSNGSLEGLNNQEGGVCQTKTMKILMKVGQDPNSAGLPR---STDPTKRPEQEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLKYRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTNGKSSTTSPFVKDHSGSSTDG--SKAGHSSILGSEVALFAGIASGCIIFIVIIITLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG
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                                                                                 IPR001799; Ephrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
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Pred. No. 1.1e-32;
2; Mismatches 125
                                                                                                           mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CEL5-L).
               Glycoprotein;
                                                                                                                                                                                                                                                          protein.
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Best Local S
Matches 146
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DISULFID
DISULFID
SEQUENCE
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CHAIN
TOPO DOM
TRANSMEM
                                                                                                                                                                             Name=efnb2a; Synonyms=efnb2;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
10-MAY-2005 (Rel. 47, Last annotation
MEDLINE-21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281; Chan J. Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B., Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T. "Morphogenesis of prechordal plate and notochord requires inta eph/ephrin b signaling.";
                                                                                                      Durbin L., Brennan C., Shiomi K., Cooke
Shanmugalingam S., Guthrie B., Lindberg
"Eph signaling is required for segmentat
                                                                                                                                                                                                                                                  Ephrin-B2a precursor.
                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=98438455; PubMed=9765210;
                                                                                                                                                                                                                                                                                                                        BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MER---
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                                                                                  12:3096-3109(1998)
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Pred. No. 1.4e:
50; Mismatches
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Ephrin-B1.
Extracellular
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By similarity.
48AF556E9ED56CD5
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PDZ recognition motif (Potential).
N-linked (GlcNAc. . .) (Potential).
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                                                                                                      K., Cooke J.,
Lindberg R.,
r segmentation
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RESULT 15
Q90Z33 BRARE
ID Q90Z33 BRARE I
AC Q90Z33;
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Best Local S
Matches 145
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EMBL; AF375225; AAK64275.1; -;
HSSP; P52800; 1IKO.
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PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Differentiation;
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SIMILARITY: Belongs to the ephrin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGVEYYKLYMVPLEQLKSCQVTKADTPLLNCVKPDQDVKFTLKFQEFSPNLWGLEFFRGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVLVIACKVNLSRALILDSIYWNTTNTKFVPGQGLVLYPQIGDKMDIVCPRVE---GGSM
                                                                                                                                                                                                                                           LRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                                                                                                                                                                          VFL--LLKYRRRHRKHS-PQHATTLSLSTLATPKRGGS----
                                                                                                                                                                                                                                                                                                                                                                  AGAGGAMCWRRRRAKPSESRHPGPGSFG-----RGGSLGLGGGGGMGPREAEPGELGIA
                                                                                                                                                                                                                                                                                                                                                                                                                              KDSKSNEVLKPDASPHGEDK--GDGNKSSSVIGSEVAL----FACIASASVIVIIIIML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHS----LEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYYIISTSNGTMEGLDNQEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPPKHPDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
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                                  PRELIMINARY;
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Cytoplasmic (Potential).

PDZ recognition motif (Potential).

PDZ recognition motif (Potential).

PDZ recognition motif (Potential).

PDZ recognition motif (Potential).

Potential (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).
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Pred. No. 1.8e-
54; Mismatches
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EMBL, AF375224; AAK64274.1; -; mRNA.
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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MEDLINE=21290827; Po
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NCBI_TaxID=7955;
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PRINTS; PR01347; EPHRIN.
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Ensembl; ENSDARG00000007723; Danio
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InterPro; IPR001799; Ephrin.
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;; PS01299; EPHRIN; 1.
E 341 AA; 37849 MW;
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                                     DPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPAAKSLESVVWNSQNPKFVSGKGLVIYPEIGDKLDIICPK----GDMGRP-YEFYKLYL
                                                                                                           LLLKLRKRTR----KHSQP----RGGTALSLSTLATPKGAAQAGSEPSDIIIPLR---TT
                                                                                                                                                                                                                         GRENEVDGNGSKMPGKDTRNONNSPGSVEGIF---GSKPALFAAIGAGCVIFLLIIIILIV
                                                                                                                                                                                                                                                                                GKEN------LPGDPTSNATSR--GAEGPLPPPSMPAVAGAAG-GLALLLLGVAGAGG
                                                                                                                                                                                                                                                                                                                                       TOEGLENREGGVCSTRSMKIIMKVGODPNAPDPDLPDLPDRPYDNEIKDPTTSPSRKTER
  ENNYCPHYEKVŚGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                               AMCWRRRAKPSESRHPGPGSFGRGGSL----GLGGGGGMGPREAEPGELGIALRGGGAA
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41.8%; Pred. No. 8
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Last sequence update)
Last annotation updat
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9; Mismatches 109;
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(Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB922F20E0D93E94 CRC64;
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/cgn2 6/ptcdata/1/iaa/6_COMB.pep:*
/cgn2 6/ptcdata/1/iaa/H_COMB.pep:*
/cgn2 6/ptcdata/1/iaa/PETUS_COMB.pep:*
/cgn2-6/ptcdata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/BE_COMB.pep:*
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US-09-949-016-10967
US-09-949-016-10967
US-09-914-631-3
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US-09-914-631-3
US-09-913-130A-2
US-08-436-044-2
US-08-436-077-2
US-08-458-077-2
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US-08-460-741-2
US-08-477-240-2
US-08-635-130A-9
US-09-949-016-11189
US-08-436-044-4
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US-08-739-333-2
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US-09-949-016-6453
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             Sequence 4, Appli
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Sequence 2, Appli
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US-08-635-130A-4
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                                                                                                                                  Query Match
Best Local Simi
Matches 340;
                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08635130A Patent No. 6696557
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130A
FILLING DATE: 19-Mar-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TOTChia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESCETE: CATCHESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                    Local Similarity
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US-09-214-631-5
US-09-2949-016-9295
US-09-214-631-13
US-09-214-631-11
US-09-214-631-12
US-09-214-631-12
US-08-299-567-5
US-08-240-124-2
US-08-299-567-121-2
US-09-957-121-2
US-09-958-734-2
US-09-949-002-478
US-09-949-002-478
US-09-949-002-473
US-09-949-002-473
US-09-949-002-473
US-09-949-002-473
US-09-949-002-473
US-09-949-002-473
US-09-949-002-473
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                                                                                                                                                 Score 1850; DB 2;
Pred. No. 1.1e-148;
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disk

Result No.

Score

1841 637.5 637.5 637.5

Mismatches

0,

Gaps

60

Length Indels

340; 0

Database

Minimum DB Maximum DB

Beq paa

Sequence: Title: Perfect score:

Scoring table:

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Sequence 6076, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2070-12

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6076

LENGTH: 340

TYPE: PRI

ORGANISM: Human
RESULT 3
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Matches 340; Conserv
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                                                                                          GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10967
LENGTH: 397
TYPE: PRT
ORGANISM: Human
US-09-949-016-10967
APPLICANT: Holland, Sacha
APPLICANT: Holland, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYSOSINE KINASES
FILE REFERENCE: 1177.23USWO
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 100.0%; Score 1850; DB 2; Local Similarity 100.0%; Pred. No. 1.3e-148;
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CURRENT APPLICATION NUMBER: US/09/051,994A
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: PCT/US96/17201
EARLIER FILING DATE: 1996-10-25
EARLIER APPLICATION NUMBER: 60/007,015
EARLIER APPLICATION NUMBER: 60/007,015
EARLIER FILING DATE: 1995-10-25
UNMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
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                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: Site
; LOCATION: (166)
; OTHER INFORMATION: XBA=Arg or Gln
US-09-051-994-2
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US-09-051-994-2
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Best Local Similarity 99.,
339; Conservative
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
FILE REFERENCE: REG-341-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09051994A
                                                                                                                                                                                    Query Match
Best Local Similarity
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TYPE: PRT
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SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
                                                     LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
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Pred. No. 3
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Pred. No. 2.4e-148;
1; Mismatches 0; Indels
                                                                                                                                                                        Mismatches
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3.5e-148;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/08/635,130A
FILING DATE: 19-Mar-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNSY/AGENT INFORMATION:
NAME: TOTCChia, PhD, Timothy E.
REGISTRATION NUMBER: 96,700
REFERENCE/DOCKET NUMBER: 91001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
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US-08-635-130A-2
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Best Local
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APPLICANT: Caras, Ingrid W
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TYPE: Amino Acid
TOPOLOGY: Linear
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STATE: Californi
                                                                                                                                                                                                                                                                                               Local Similarity
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                  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
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100.0%; Pred. No. 9e-148;
ative 0; Mismatches 0;
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US-08-436-044-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-I
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436
FILING DATE: 05-MAY-1995
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bennett, Brian D. APPLICANT: Matthews, William TITLE OF INVENTION: HTK LIGAND
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REFERENCE/DOCKET NUMBER: 902D3
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                                                                                              DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
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                                GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                     GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
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 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFÄGIASGCIIFIVIIITLVVLLL 253
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EM: PC-DOS/MS-DOS
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Patent No.
                                                                                                                                                                                                                                                                                                                                              Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/436.
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
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CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                     194
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                                                                       GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                DYYTISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193
                                                                                                                                                  DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                          GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                       GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
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WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                     GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                          34.5%; Score 637.5; DB 1; 42.1%; Pred. No. 4.9e-46; ative 49; Mismatches 129;
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TOPOLOGY:
PCT-US95-08812-2
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PCT-US95-08812-2
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LENGTH: 336 amin
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            Matches 139;
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                  KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                                                                                  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                      DYYTISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193
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                                                                                             GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
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                                                                                                                                                                                                                                                                                                                                                                                                          34.5%; Score 637.5; DB 4; Length 336; ilarity 42.1%; Pred. No. 4.9e-46; Conservative 49; Mismatches 129; Indels 13;
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US-08-213-403-2
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Patent No. !
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.2%; Score 632; DB 1; Length 346; Best Local Similarity 39.5%; Pred. No. 1.5e-45; Matches 145; Conservative 48; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977
EILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 5512457el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
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232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ----
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                                                                                                                                                                                                                                                                        62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
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                                                                                                                                                                                                                                                                                                                                                   PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                    -----LLLLGVAGAGGA-------MCWRRRRAKPSESRHPGPGSFGRGGSLGL
                                                                           SRPSKEADNTVKWATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
                                                                                                               SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
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    -- RAAALSL
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US-08-458-077-2
                                                                                                                                                                                                                                           Best Local Similarity Matches 145; Conserv
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08458077 Patent No. 5627267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OBERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,077
FILING DATE: 01-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
FILING DATE: 15-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/977,693 FILING DATE: 13-NOV-1992 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washing
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ANIYYKV 346
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                                                                                 CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                                                    CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
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                                                                                                                                                              PGORWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII
                                                                                                                                                                                                    PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
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51 University Street
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                                                                                                                                                                                                                                     34.2%; Score 632; DB 1; Length 346;
39.5%; Pred. No. 1.5e-45;
ative 48; Mismatches 116; Indels 58;
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US-08-460-741-2
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                                                               Matches 145;
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                                                                            Best Local Similarity
                                                                                             Query Match
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                                                                                                                                                                                                                          TELEFAX: (206) 233-06
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                 FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: Apple Maci
                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                  TELEPHONE: 120-
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FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
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                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                        LENGTH:
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PGGVRVGALLLLIGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
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                                                                                                                                                                                        346 amino acids
                                                               Conservative
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Beckmann, M. Patricia
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                                                                                                                                                                                                                                                         (206) 587-0430
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233-0644
-- NO: 2:
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                                                           34.2%; Score 632; DB 1; I
39.5%; Pred. No. 1.5e-45;
htive 48; Mismatches 116;
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o. 5670625el Cytokine Designated elk Ligand
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                                                                                             Length 346;
                                                               Indels
                                                               58;
                                                               Gaps
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; TOPOLOGY: 15; MOLECULE TYPE: US-08-747-240-2
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US-08-747-240-2
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                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,240
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (268) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                    TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple SySOPRARE: Microsca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 98101
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                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL
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                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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                                                                                                                                                                                                                                                                                                                                                                                                              Apple System 7.1
Et Word for Apple,
                                                                                                                                                                                                                                                                                                                                                                                                                 Version 5.1a
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RESULT 14
US-08-299-567-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Davis,
                                                                                                                                TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                          APPLICATION NUMBER: US/08/299
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
STRANDEDNESS:
TOPOLOGY: unl
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10591-6707

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM FC compatible

OBERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 346 amino acid
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                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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777 Old Saw Mill River Road
                                                                                      346 amino acids
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APPLICANT: Backmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa K.
ITITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
FILE REFERENCE: GENERT: 67CPDV3
CURRENT APPLICATION NUMBER: US/09/039,642B
CURRENT FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 08/213,403
PRIOR APPLICATION NUMBER: 07/97,693
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR APPLICATION NUMBER: 08/747,240
PRIOR APPLICATION NUMBER: 08/747,240
PRIOR FILING DATE: 1996-10-12
PRIOR APPLICATION NUMBER: 08/747,240
PRIOR FILING DATE: 1995-06-02
NUMBER OFTENING DATE: 1995-06-02
NUMBER OF SEO ID NOS: 5
SOPTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 2
LENGTH: 346
TYPE: PRT
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US-09-039-642B-2
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Best Local Similarity
Matches 145; Conserv
                                                                                                                 Query Match 34.2%; Score 632; DB 2; Length 346; Best Local Similarity 39.5%; Pred. No. 1.5e-45; Matches 145; Conservative 48; Mismatches 116; Indels
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Patent No. 6540992
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                                                                                                                                                                                                       -09-039-642B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
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  CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS
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                                       PĠQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                             PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
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 ANIYYKV 346
                                                            STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
                                                                                ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                          GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALSL
                                                                                                                                                        -----LLLLGVAGAGGA-------MCWRRRRAKPSESRHPGPGSFGRGGSLGL
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Search completed: December 21, 2005, 14:37:39 Job time: 28.7987 secs

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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1482.921 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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US-10-021-121-4
US-10-723-660-4256
US-10-698-907-16
US-10-698-907-8
US-10-698-907-8
US-10-698-907-7
US-10-698-907-7
US-10-698-907-7
US-10-698-907-14
US-10-698-907-14
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US-10-698-907-18
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US-10-698-639-62
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US-10-138-787-5
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             sequence 3, Appli
Sequence 2, Appli
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Sequence 7, Appli
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Sequence 9, Appli
Sequence 60, Appli
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Sequence 5, Appli
Sequence 61, Appli
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Sequence 4256, Ap
Sequence 16, Appli
Sequence 3, Appli
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9.7	9.7	9.7	9.8	9.8	10.8	10.8	10.9	10.9	10.9	11.1	15.4	23.9	23.9	23.9	24.1	24.1	24.2
238	238	238	652	652	82	82	82	82	106	136	92	233	233	226	459	459	229
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US-10-241-220-72	US-09-733-756-2	US-09-904-954-2	US-11-097-143-23436	US-11-097-143-2655	US-10-138-787-12	US-09-862-179A-16	US-10-138-787-11	US-09-862-179A-15	US-09-925-297-639	US-09-864-761-48257	US-09-864-761-48262	US-10-800-077-388	US-10-800-350-388	US-10-698-907-21	US-10-800-077-390	US-10-800-350-390	US-10-698-907-20
Sequence 72, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 23436, A	Sequence 2655, Ap	Sequence 12, Appl		Sequence 11, Appl	Sequence 15, Appl	Sequence 639, App	7	•	Sequence 388, App		Sequence 21, Appl	Sequence 390, App	$\overline{}$	Sequence 20, Appl

ALIGNMENTS

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RESULT 1

US-10-021-121-4

US-10-021-121-4

Sequence 4, Application US/10021121

Sequence 4, Application US/10021121

Publication No. US20020142444A1

GENERAL INFORMATION:
APPLICANT: Carras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
ADDRESSE: Genentech, Inc.
                                                                                                                                                                   LENGTH: 340 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4
                                                                                      Query Match
Best Local S
Matches 340
                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (denentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/021,121

FILING DATE: 06-Dec-2001

CLASSIFICATION - CURKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/635,130

FILING DATE: 19-Max-1996

ATTORNEY/AGENT INFORMATION:

NAME: TOSCHIA, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 36,700

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8874

TETERPHONE: 650/225-9871
                                                                                                           Local Similarity
                                                                                        340;
1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYMNSANKRFQAEGGYVLYPQIGDRLDL 60
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STATE: California
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                                                                                        Conservative
                                                                                 100.0%; So
100.0%; P:
ative 0;
                                                                                      Score 1850; DB 4; Length 340; Pred. No. 3.5e-131; Mismatches 0; Indels 0
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US-10-723-860-4256
Sequence 4256, Application US/10723860
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 4256
LENGTH: 340
TWORD: DDM
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Matches 340;
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ORGANISM: Homo sapiens
-10-723-860-4256
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                      GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR PRIOR PRIOR PRIOR WIMBER: US 10/291,290
PRIOR PRIOR PRIOR DATE: 2002-11-08
PRIOR PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR PRIOR PRIOR NUMBER: US 60/345,206
PRIOR PRIOR PRIOR DATE: 2002-07-02
PRIOR PRIOR PRIOR DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 16
LENGTH: 340
TYPE: PRT
ORGANISM: Homo mapiens
Sequence 3, Application US/10138787

Publication No. US20020172984A1

GENERAL INFORMATION:

APPLICANT: Holland, Sacha
APPLICANT: Mommalu, Geraldine
APPLICANT: Mommalu, Geraldine
APPLICANT: PAWSON, TONY

TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787

CURRENT APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
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US-10-698-907-16
Sequence 16, Application US/10698907
Deblication No. US20050049194A1
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US-10-138-787-3
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Best Local S
Matches 340
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APPLICANT: Frisen, Jonas
APPLICANT: Frisen, Jonas
APPLICANT: Holmberg, Johan
TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
TITLE OF INVENTION: Proliferation
FILE REFERENCE: 21882-529 UTIL
CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT FILING DATE: 2003-10-31
CURRENT FILING DATE: 2003-10-31
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APPLICANT: Samuel Davis, et al.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
FILE REFERENCE: REG-341Z
CURRENT APPLICATION NUMBER: US/10/417,924A
CURRENT APPLICATION NUMBER: US/00/417,924A
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: 09/651,994
PRIOR FILING DATE: 1998-04-24
PRIOR FILING DATE: 1998-04-24
PRIOR FILING DATE: 1998-01-25
PRIOR APPLICATION NUMBER: PCT/US96/17201
PRIOR APPLICATION NUMBER: BOJ/007,015
PRIOR FILING DATE: 1995-10-25
INUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 340
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10417924A Publication No. US20030215918A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
Matches
                                       Query Match
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Best Local (
                                                                  PEATURE:
NAME/KEY: Misc. feature
LOCATION: (166)
OTHER INFORMATION: Xaa = unknown or other
-10-417-924A-2
                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Bapiens
                Match 99.7%; Score 1844; DB 4; Length 340; Local Similarity 99.7%; Pred. No. 9.9e-131;
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Similarity 99.7%;
39; Conservative
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1 MGPPHSGPGGVRVGALLLLLGVLGLVSGLSLEPVYMNSANKRFQAEGGYVLYPQIGDRLDL

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TELEPHONE: 650/952-8674

TELEPAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-021-121-2
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US-10-021-121-2
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   Matches 338;
                     Query Match
Best Local Similarity
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APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Mar-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Genentech, Inc.
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                                                                                                                                                                                                                                                            NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: P1001
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                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San
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   99.5%;
llarity 100.0%;
Conservative (
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Score 1841; DB 4;
; Pred. No. 2.3e-130;
0; Mismatches 0;
                                                                                              N
                                    Length 455;
     Indels
     0;
     Gaps
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CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT PILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR FILING DATE: 2002-07-02
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
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US-10-698-907-8
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Publication No. US20050049194A1
GENERAL INFORMATION:
APPLICANT: Frisen, Jonas
APPLICANT: Holmberg, Johan
TITLE OF INVENTION: Use of Ephrins and Related
TITLE OF INVENTION: Proliferation
                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 340
TYPE: PRT
ORGANISM: Mus :
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                                                                                                                                                                                                                                                                                                                                                                                325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
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                                                                                 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                      MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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                                                                                                                                                                                                                  LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                                                                                                                       LCPRARPBGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
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                      GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
                                                           VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL
                                                                                                                                      SPNLWGHEFRSHHDYYLIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
                                                                                                                                                                                                                                                                                                  MGAPHFGPGGVQVGALLLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                              96.2%;
95.6%;
                                                                                                                                                                                                                                                                                                                                                                            Score 1780; DB 5;
Pred. No. 6.6e-126;
7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
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Sequence 7, Application US/10698907; Publication No. US20050049194A1; GENERAL INFORMATION:

APPLICANT: Frisen, Jonas
APPLICANT: Holmberg, Johan
TITLE OF INVENTION: Use of Ephrins and Related Molecules
TITLE OF INVENTION: Proliferation
FILE REFERENCE: 21892-529 UTIL
CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR FILING DATE: 2003-04-03
PRIOR FILING DATE: 2002-11-08

to Regulate Cellular

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APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEON
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATS: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2695
LENGTH: 285
TYPE: PRT
ORGANISM: Homo sapiens
RESULT 9
US-10-698-907-7
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US-10-408-765A-2695
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ghosh, Soumitr
APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           % Match 84.3%; Score 1559; DB 4; 1
Local Similarity 100.0%; Pred. No. 2.4e-109;
1es 285; Conservative 0; Mismatches 0;
                                                                                   241
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                                                                                                                ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                               ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI
                                                                                                                                                                                                                                                                                 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
                                                                                                                                                                                                                                                                                                                                          KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA
                                                                                                                                                                                                                                                                                                                                                                    KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                              DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI
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                                                                                 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 285
                                                                                                                                                                       ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI
                                                                                                                                                                                                                                                        VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
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RESULT 10
US-10-021-121-9
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-698-907-7
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PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10021121 Publication No. US20020142444A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
34.5%; Score 637.5; DB 5;
Best Local Similarity 42.1%; Pred. No. 8e-40;
Matches 139; Conservative 49; Mismatches 129:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/021,121

FILING DATE: 06-Dec-2001

CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:

APPLICATION UNMBER: US/08/635,130

FILING DATE: 19-Mar-1996

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
NAME: Torchia, PhD., Timothy E
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genente
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Fr
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech,
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                  94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Francisco
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SEQUENCE CHARGTERISTICS:
LENGTH: 346 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-021-121-9
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; ORGANISM: Homo US-10-356-289-2
                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/09/039,642B
PRIOR FILING DATE: 1998-03-16
PRIOR PPLICATION UMBER: 08/213,403
PRIOR FILING DATE: 1994-03-15
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR FILING DATE: 1992-11-13
PRIOR FILING DATE: 1992-11-13
PRIOR FILING DATE: 1996-10-12
PRIOR FILING DATE: 1996-10-12
PRIOR FILING DATE: 1996-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-356-289-2
                                                                          NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10356289 Publication No. US20040022767A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: GENENT.67CPDV3
CURRENT APPLICATION NUMBER: US/10/356,289
CURRENT FILING DATE: 2003-01-31
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Carpenter, Melissa K.
TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lyman, APPLICANT: Beckma
                                                                                                                                     PRIOR APPLICATION NUMBER: 08/460,741 PRIOR FILING DATE: 1995-06-02
                                     LENGTH: 346
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Baum, Peter R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart D.
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Sequence 60, Application US/10712124

Publication No. US20040146907A1

GENERAL INFORMATION:
APPLICANT: SMITH, VICTORIA

FILE REFERENCE: P2000R1

CURRENT APPLICATION NUMBER: US/10/712,124

CURRENT FILING DATE: 2003-11-13

PRIOR PILING DATE: 2002-11-13

CURRENTHING DATE: 2002-11-13

PRIOR PILING DATE: 2002-11-13

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US-10-712-124-60
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Best Local
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                                     SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                               PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT
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US-10-789-378-30
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CURRENT APPLICATION NUMBER: US/10/789,378
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: 10/441925
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60/381619
PRIOR APPLICATION NUMBER: 60/381619
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/450886
PRIOR FILING DATE: 2003-02-26
NUMBER OF SEQ ID NOS: 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.2%; Score 632; DB 5; Length 346; Best Local Similarity 39.5%; Pred. No. 2.2e-39; Matches 145; Conservative 48; Mismatches 116; Indels
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SEQ ID NO 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Axenovich, Sergey
APPLICANT: Stull, Robert
APPLICANT: Gelman, Marina
APPLICANT: Chui, Kitty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ng, Dean TITLE OF INVENTION: DIAGNOSTIC METHODS FOR CANCER DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
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                                       PNIYYKV 340
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                                                                                 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
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RESULT 14 US-10-698-907-14

Sequence 14, Application US/10698907 Publication No. US20050049194A1

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RESULT 15
US-09-754-105-2
J Sequence 2. Application US/09754105
Patent No. US20010009768A1
J GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas
APPLICANT: Reddy, Pranhitha
APPLICANT: Reddy, Pranhitha
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
FILE REFERENCE: 2823
CURRENT APPLICATION NUMBER: US/09/754,105
CURRENT FILING DATE: 2001-01-03
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PRIOR PILING DATE: 2003-04-03
PRIOR PELICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2001-11-09
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SOFTWARE: PatentIn ver
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.2%; Score 632; DB 5; Length 346; Best Local Similarity 39.5%; Pred. No. 2.2e-39; Matches 145; Conservative 48; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Holmberg, Johan TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular TITLE OF INVENTION: Proliferation FILE REFERENCE: 21882-529 UTIL CURRENT APPLICATION NUMBER: US/10/698,907 CURRENT FILING DATE: 2003-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Frisen, Jonas APPLICANT: Holmberg, Jol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LLLLGVAGAGGA-------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
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; LENGTH: 333
; TYPE: PRT
; ORGANISM: homo sapiens
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PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.0
Best Local Similarity 40.9
Matches 135; Conservative
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                             YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                             YRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                            WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                              GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC 250
                                                                                                                                                                                              DYYTISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
                                                                                                                                                                                                                   DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                                                                               GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFÄGIASGCIIFIVIIITLVVLLL
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40.9%; Pred. No. 3.2e-39;
vative 52; Mismatches 130;
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Search completed: December 21, Job time : 96.7987 secs 2005, 14:41:51 THIS PAGE BLANK (USPTO)

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*
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 US-10-949-720-396
US-10-949-720-390
US-10-949-720-380
US-10-131-826A-288
US-10-131-826A-288
US-11-186-284-35
US-11-186-284-35
US-11-186-284-33
US-10-821-234-1431
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US-10-821-234-1096
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US-10-821-234-1096
US-10-821-234-1096
US-10-955-561-914
US-10-955-561-915
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US-10-995-561-910
US-10-995-561-911
US-10-995-561-913
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Sequence 396, App
Sequence 390, App
Sequence 388, App
Sequence 288, App
Sequence 53, Appl
Sequence 35, Appl
Sequence 37, Appl
Sequence 964, App
Sequence 964, App
Sequence 914, App
Sequence 914, App
Sequence 914, App
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 911, App
Sequence 911, App
Sequence 911, App
Sequence 911, App
Sequence 912, App
Sequence 913, App
Sequence 933, App
Sequence 932, App
Sequence 933, App
Sequence 933, App
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99	99	99.5	101.5	102	103.5	104.5	104.5	104.5	107	111	112	113.5	114	114	114	116.5	116.5	116.5	116.5
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US-10-802-796-728	US-10-802-796-727	US-11-085-775-3	US-11-102-240-16	US-11-110-424-4	US-10-995-561-786	US-10-821-234-1688	US-10-477-507A-2	US-10-477-507A-4	US-11-107-028-26	US-10-848-976-1	US-10-857-780-20	US-10-995-561-987	US-10-995-561-982	US-10-995-561-981	US-10-995-561-983	US-10-995-561-991	US-10-995-561-989	US-10-995-561-990	US-10-995-561-988
Sequence 728, App	Sequence 727, App	Sequence 3, Appli	Sequence 16, Appl	Sequence 4, Appli	Sequence 786, App	Sequence 1688, Ap	Sequence 2, Appli	Sequence 4, Appli	Sequence 26, Appl	Sequence 1, Appli	Sequence 20, Appl	Sequence 987, App	-	-	Sequence 983, App	-	-	Sequence 990, App	•

TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH FILE REFERENCE: VASG-PO2-002 CURRENT APPLICATION NUMBER: US/10/949,720 CURRENT FILING DATE: 2004-09-23 PRIOR APPLICATION NUMBER: US 60/454,432 PRIOR APPLICATION NUMBER: US 60/454,330 PRIOR APPLICATION NUMBER: US 60/454,300 PRIOR FILING DATE: 2003-03-12 PRIOR APPLICATION NUMBER: US 10/800,350 PRIOR FILING DATE: 2003-03-12 PRIOR APPLICATION NUMBER: US 10/800,350 PRIOR FILING DATE: 2004-03-12 NUMBER OF SEQ ID NOS: 425 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 396 LENGTH: 333 TYPE: DATE: ; Sequence 396, Application US/10949720 ; Publication No. US20050249736A1 ; GRNERAL INFORMATION: ; APPLICANT: Krasnoperov, Valery ; APPLICANT: Zozulya, Sergey ; APPLICANT: Kertesz, Nathalie ; APPLICANT: Reddy, Ramachandra ; APPLICANT: Gill, Parkash

US-10-949-720-396

ALIGNMENTS

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								Matches 135; Conservative 52; Mismatches 130;	Query Match 34.0%; Score 629.5; DB 6;
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191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIITLVVLLL 250	191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250	131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190	134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER-DR 190	71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130	74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133	70	73	۷n	
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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-949-720-396

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CURRENT APPLICATION NUMBER: US/10/949,720
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/454,432
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
PRIOR FILING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FRANSEQ for Windows Version 4.0
SEQ ID NO 390
LENGTH: 459
TYPE: PRT
ORGANISM: Unknown
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                RESULT 3
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; OTHER INFORMATION: Recombinant B2EC-FC protein US-10-949-720-390
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APPLICANT: Krasnoperov, Valery
APPLICANT: Krasnoperov, Valery
APPLICANT: Cozulya, Sergey
APPLICANT: Kertesz, Nathalie
APPLICANT: Reddy, Ramachandra
APPLICANT: Gill, Parkash
TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
EILE REFERENCE: VASG-PO2-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 390, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                   192
                                                                                                                                                                                                                                                                                                                                   194
                                                                                                                                                                                                                                                                                                                                                                                                 134 DYYIIATSDGTREGLESLQCGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                           238
                                                                                                                                                                                                                                            254 RRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                       -PFCPHYEKVSG 316
                                                                                                                                                                                                                                                                                                                                     HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                              CPPCPAPELLGG 249
                                                                                                                                                                                                                                                                                                                                                                               DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                RSSTTSPFVKPNPGSSTDGNSAGHSGNNILG-SEVDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10949720 D. US20050249736A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.1%; Score 446.5; DB 6
33.7%; Pred. No. 4.5e-28;
tive 39; Mismatches 83
                                                                                                                                                                                                                                                                                          -DASSAGSTRNKDPTRRPELE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
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CURRENT APPLICATION NUMBER: US/10/949,720
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/454,432
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/454,300
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR ELING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 388
                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-131-826A-288
; Sequence 288, Application US/10131826A
; Publication No. US20050245730A1
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity
Matches 97; Conserv
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zozulya, Sergey
APPLICANT: Kertesz, Nathalie
APPLICANT: Reddy, Ramachandra
APPLICANT: Gill, Parkash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Krasnoperov, Valery
APPLICANT: Zozulya, Sergey
APPLICANT: Kertesz, Nathalie
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APPLICANT
                        APPLICANT
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ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 RRAKPSESRHPGPGSFGRGGSLGLGGGGGMG 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                       Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
                                                                                                                                                                                                                                                              Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                           RSSTTSPFVKPNPGSSTDGNSAGHSGNNILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYYTISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQ--
                                                                                                                   Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
                  Stewart, Timothy A.
                                                                                                                                                                               Filvaroff, Ellen
                                                                                                                                                                                                      Desnoyers, Luc
                                                                                                                                                                                                                        DeForge, Laura
    Tumas,Daniel
                                                                                                                                                                                                                                             Beresini,Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.9%; Score 442; DB 6; ilarity 35.8%; Pred. No. 4.7e-28; Conservative 36; Mismatches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                             222
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RESULT 5
US-10-220-824-8
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                                            NUMBER OF SEQ ID NOS: 16
SOFTWARE: Kopatentin 1.71
SEQ ID NO 8
LENGTH: 1516
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10220824
Publication No. US20050277603A1
GENERAL INFORMATION:
APPLICANT: ViroMed Limited
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SEQ ID NO 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
ORGANISM: Homo sapiens
-10-220-824-8
                                                                                                                                                                   TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including TITLE OF INVENTION: gene encoding an anti-angiogenic protein or parts thereof FILE REFERENCE: OPF0208/PCT CURRENT APPLICATION NUMBER: US/10/220,824 CURRENT FILING DATE: 2002-08-30 PRIOR APPLICATION NUMBER: KR 2001-0000691 PRIOR APPLICATION NUMBER: KR 2001-0000691 PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapien
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APPLICATION NUMBER: 60/059352
FILING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/059588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHDNPQE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSADAAM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%; Score 164.5; DB 6;
27.7%; Pred. No. 1.8e-06;
tive 31; Mismatches 74;
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                                                                                                                 Matches
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                     SEQ ID NO 35
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Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSME
TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-05-20
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/381,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                         LENGTH: 1496
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                               y Match 7.7%; Score 142.5;
Local Similarity 29.1%; Pred. No. 0.00
hes 55; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/361,978 FILING DATE: 2002-03-05
218 GPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP----GSFGRGG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
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                                                                         169 QSPRG--GAV-PRKPVSEMPMERDRGAAHSLEPGKENLPG-----DPTSNATSRGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           809 DG-PQGPPGL 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                     RGPRGDPGTLGPPGPVGERGAPGNRGF----PGSDGLPGPKGAQGERGPVGSSGPKGSQ
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Monahan, John E.
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Guillemette, Tra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%; Score 144.5; DB 6; 23.5%; Pred. No. 0.00062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2005-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                   .5; DB 7;
0.00088;
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                                                                                                                                                     Length 1496
                                                                                                                 Indels
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US-11-186-284-37
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SEQ ID NO 37
LENGTH: 744
TYPE: PRT
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Best Local
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APPLICANT: Burgart, Lawrence J.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEMOI-02992RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
CURRENT FILING DATE: 2005-07-21
DRIOR APPLICATION NUMBER: US/10/301,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
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  330
                                       362
                                                                              275 LGLGG-GGGMGPREAEPGELGIALRGGGAADP--PFCPHYEKVSGDYGHPVYIVQDGP--
                                                                                                                                                             242 VAGAGGAMCWRRRRAKPSESRHPG------
                                                                                                                                                                                                     257 ----PGMHGL-PGPVGLPGVGKPGVTGFPGPQGPLGKPGAPGEPGRQGPIGVPGVQGPPG
                                                                                                                                                                                                                                          187 ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL----G
                                                                                                                                                                                                                                                                                                                                                                 198 PPGPHGLPG-----IGKPGGPGLPGQPGPK---
                                                                                                                                                                                                                                                                                                                       127 HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM
                                                                                                                                                                                                                                                                                                                                                                                                      67 PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                         RGMGGVPGALGPR-GEKGPIGSPGIGGSPGEPGLPGIP-----GPMGPPGAIGFPGPKG
                                                                                                                    IPGIG-----KPGQDGIPGQPGFPGGKGEQGLPGLPGAPGLPGIGKPGFPGPKGD
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Schlegel, Robert
Monahan, John E.
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23.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 142; DB 7;
Pred. No. 0.00044;
6; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 744;
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILTE OF INVENTION: THERAPY OF COLON CANCER
FILTE REFERENCE: MPMO1-029P2RNM
CURRENT FILLING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/11/186,284
CURRENT FILLING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/60/301,822
PRIOR APPLICATION NUMBER: US/60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,988
PRIOR APPLICATION DATE: 2002-05-20
PRIOR APPLICATION DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
COFFERENCE: CONTROL OF SEC 
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US-11-186-284-39
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SEQ ID NO 39
LENGTH: 744
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Publication No. US20050266493A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 72; Conserv
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APPLICANT:
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ORGANISM: Homo Sapiens
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GIVGPQGPP 425
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                                                            ----PQSPP 334
                                                                                                                                                                                            LGLGG-GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGP----
                                                                                                                            RGMGGVPGALGPR-GEKGPIGAPGIGG----PPGEPGLPGIPGPMGPPGAIGFPGPKGEG
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Schlegel, Robert
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Guillemette, Tracy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 23.3%;
Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IGKPGGPGLPGQPGPK----
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23.3%; Pred. No. 0.00044;
lve 16; Mismatches 99; Indels 1
                                                                                                                                                                                                                                                           -KPGQDGIPGQPGFPGGKGEQGLPGLPGPPGLPGIGKPGFPGPKGD
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; Sequence 964, Application US/10821234 ; Publication No. US20050255114A1 ; GENERAL INFORMATION:

APPLICANT: Labat, Ivan

US-10-821-234-964

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US-11-186-284-33
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 964
LENGTH: 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/11186284
Publication No. US20050266493A1
                                                                                          SOFTWARE: F
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEMO1-029PZNMM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILLING DATE: 2005-07-21
                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Millennium Pharmaceuticals, APPLICANT: Berger, Allison
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/10/301,822 PRIOR FILING DATE: 2002-11-21
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TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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ORGANISM: Homo sapiens
                     ORGANISM: Homo Sapiens
                                                                 LENGTH:
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                                                                                                               FastSEQ
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Schlegel, Robert
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Andarmani, Susan
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                                                                                                                  for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1182, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: pt_SEQ_genes Version 1.0
SEQ_ID_NO 1182
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1874
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                     602 LTGRPGPVGPPGS-----GGLKGEPGDVGPQGPRGVQGPPGP-----AGKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              964 MPGPRGSPGPQGVKGESGKPGANGLSGERGPPGPQGLPGLAGTAGEPGRDGNPGSDGLPG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 PRGGAVPRKPVSEMPMERDRGA----AHSLEPGKENLPGDPTSNAT-----SRGAEG
                                                                                                                                                                                                                                                                                                                                                                                                        61 LCPRARPPGPHSSPNYEFYKLYLVGGAQG-----RRCEAPPAPNLLLTCDRPDLD 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                   EGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSL
PGEKGGQGPP 816
                                                                        GLPGPQGAIGP---
                                                                                                           GL-GGGGGMGPREAEPGELGIALRGG-----GAADPPFCPHYEKVSGDYGHPVYIVQDGP
                                                                                                                                               LGPKGPPGPPGPPGVTG-
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                                    QSPP
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                                                                          PGEKGPLGKPGLPGMPGADGPP-
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                                                                                                                                               -MDGQPGPKGNV
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                                                                          -GHP---GKEGP
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FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 914
LENGTH: 1532
                                                                                                                      FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1431
LENGTH: 1366
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                                                              US-10-821-234-1431
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1431, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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Matches
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens -10-821-234-914
                                                                                                                                                                                                                                                                                                                 APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stache-Crain, Birgit
                                                                                ORGANISM: Homo sapiens
                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 LRGGGAA-------DPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 LILGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSLGLGGGGGGMGPREAEPGELGIA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        741 PGPKGDQGEKGPRGLTG--EPGMRGLPG-AVGEPGAKGAMGPAGPDGHQGPRGEQG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 RKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLAL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684 AGEPGPHGPPG-----VPGSVGPKGSSGSPGPQGPPGP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 ARPPGPHSSPNYEFYKLYLVGGAQGRR-----CEAPPAPNLLLTCDRPDLDLRFTIKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 135.5; DB ilarity 23.5%; Pred. No. 0.0032; Conservative 18; Mismatches 10
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7.3%;
25.3%;
Score 134.5; DB Pred. No. 0.0033;
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                      Length 1366;
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US-11-186-284-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILLING DATE: 2002-11-21
PRIOR PELICATION NUMBER: US 60/339,971
PRIOR PILLING DATE: 2001-12-10
PRIOR PILLING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILLING DATE: 2002-05-20
PRIOR FILLING DATE: 2002-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                      Matches
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE DEPENDENCE. THERAPY OF COLON CANCER
ETITE DEPENDENCE. THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 APGPDGNNGAQGPPGPQGV--QGGKGEQGPAGPPGFQGLPGPSGPAGEVGKP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 PGLPGPRGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGEPGSAG----PQ-----
370 -----GPPGP-----
                                                                                         321 PGLPGPRGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGEPGSAG----PQ-----
                                           61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-----CEAPPAPNLLLTCDRPDLDLRF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-----CEAPPAPNLLLTCDRPDLDLRF 113
                                                                                                                                                                                   89;
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                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version
                                                                                                                                   PPHSGPGGV--RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guillemette,
                                                                                                                                                                              7.3%; Score 134.5; DB 7; ilarity 25.3%; Pred. No. 0.0033; Conservative 14; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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--SGEEGKRGPNGEAGSAGPPGP----
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                                                                                                                                                                                      Indels 135;
                                                                                                                                                                                                                               Length 1366;
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR APPLICATION NUMBER: US/0/309,971
PRIOR APPLICATION NUMBER: US 60/319,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-05-05
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-05
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-20
NUMBER: OF SEO ID NOS. 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-28
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1464
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.2%; Score 133; DB 7; Length 1464; Best Local Similarity 25.8%; Pred. No. 0.0047; Matches 99; Conservative 19; Mismatches 128; Indels 13
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                                                  160 GMKVLLRVG-----QSPRGGAVPRKPVSEM-----PMERDRGAAHSLE--PGKENLP 204
                                                                                                                                                                 107 PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT--REGLESLQGGVCL----TR 159
                                                                                                                                                                                                                            887 GPSGNAGPPGPPGPAGKE------GGKGPRGETGPAGRPGEVGPPGPPGP-----
                                                                                                                                                                                                                                                                                                                                              848 GPP--GPIG-NVGAPGAKGARG-----SAGP-----PGATGFPGAAGRVGPP 886
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                                                                                                                                                                                                                                                                                  62 CP--RARPPGPHSSPNYEFYKLYLVGGAQGRRCE------APPAPHLLLTCDR 106
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GFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAPAAEGSPGRDGSP
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Monahan, John E.
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Search completed: December 21, 2005, 14:55:35 Job time : 7.41509 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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US-08-436-044-2
US-08-436-044-2
US-08-436-044-2
US-08-436-077-2
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Sequence 2, Application US/08635130A
Patent No. 6696557
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Result No.

Database

Maximum Minimum Total number

80

Sequence:

ALIGNMENTS

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Query Match 100.0%; Sest Local Similarity 100.0%; Featches 455; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flopp:
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130A
FILING DATE: 19-Mar-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                      TYPE: Amino acids
TYPES: Amino Acid
TOPOLOGY: Linco
                                                                                                                                                                                                                                                                                                                                                       NAME: Torchia, PhD., Timothy E
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                             MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                            MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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Pred. No. 1.9e-199;
; Mismatches 0;
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Best Local Similarity
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Patent No. 6696557
GENERAL INFORMATION:
                                                                                                                    Matches 338;
                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TORCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/OFILING DATE: 19-Mar-1996
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CITY: South San Francisco
                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                   H: 340 amino acids
Amino Acid
LCPRARPDGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
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                                                                    MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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                                                     MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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                                                                                                                    Conservative
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                                                                                                                 75.1%; Score 1841; DB 2; 1 100.0%; Pred. No. 5.5e-148; tive 0; Mismatches 0;
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/247,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,758
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; ORGANISM: Human
US-09-949-016-6076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6076, Application US/09949016 Patent No. 6812339
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Similarity 100.0%; Pred. No. 5.5e-148;
38; Conservative 0; Mismatches 0;
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                                           GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY
                                                                                                                   GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
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Sequence 10967, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-010-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10967
LENGTH: 397
TYPE: PRT
ORGANISM: Human
US-09-949-016-10967
GENERAL INFORMATION:

APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: BY INFORMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
TITLE OF INVENTION NUMBER: US/09/214,631
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1997-07-04
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
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US-09-214-631-3
; Sequence 3, Application US/09214631
; Patent No. 6413730
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US-09-949-016-10967
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-631-3
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                                                           片
                                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: site
LOCATION: (166)
OTHER INFORMATION: Xaa=Arg or Gln
US-09-051-994-2
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/051,994A
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: PCT/US96/17201
EARLIER FILING DATE: 1996-10-25
EARLIER APPLICATION NUMBER: 60/007,015
EARLIER APPLICATION NUMBER: 60/007,015
EARLIER FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
Matches 337; Conserv
                                                                                                                                  Matches
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: REGENERON PHARMACEUTICALS, INC. TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FILE REFERENCE: REG-341-PCT-US
                                                                                                                                                                                                                                                                                                   TYPE: PRT
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               LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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                                                              MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                 Conservative
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99.7%;
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Pred. No. 1.2e-147;
                                                                                                                                                Score 1835; DB 2;
Pred. No. 1.8e-147;
                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY LIGANDS
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                                                                                                                                                                Length 340;
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US-08-436-044-2
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
                                                                                                                                   Matches 137;
                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08436044 Patent No. 5624899
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APPLICANT: Bennett, Brian D.
APPLICANT: Matthews, William
TITLE OF INVENTION: HTK LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 20-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                   TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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               74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLMGHEFRSHH 133
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                                                                                   GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
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GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                               GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                   Score 628.5; DB 1;
Pred. No. 3.3e-45;
                                                                                                                                   Mismatches
                                                                                                                                   129;
                                                                                                                                                                   Length 336;
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RESULT 8
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                                                                                                                                                                        Query Match
Best Local Similarity
Matches 137; Conserv
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Patent No. !
                                                                                                                                                                                                                                                                                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 5.25 inv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bennett, Brian D. APPLICANT: Matthews, William TITLE OF INVENTION: HTK LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01 FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05 CLASSIFICATION:
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134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                     74
                                                        74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQBYSPNLWGHEFRSHH 133
                                                                                                           17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                                                                  14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
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                                   GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
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                                                                                                                                                                                25.7%; Score 628.5; DB 1; ilarity 41.8%; Pred. No. 3.3e-45; Conservative 49; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B: 5.25 inch, 360 Kb floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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PCT-US95-08812-2
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                                                                                                                                                                                                              Matches 137;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 336 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HTK LIGAND NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech,
                                                                                                                                                                                                                                                                                                TYPE: amd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc
STREET: 460 Point San Bru
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                  134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
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                                                                                                                                        17
                                                                                                                                                                         14
                                                                                        74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application PC/TUS9508812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                    GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEKVSGDYGHPVYIVQEMPPQSPANIYY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          25.7%; Score 628.5; DB 4;
41.8%; Pred. No. 3.3e-45;
/ative 49; Mismatches 129;
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                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                             Length 336;
                                                                                                                                                                                                              13;
                                                                                                                                                                                                            Gaps
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US-08-213-403-2
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Patent No. 5
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Lyman,
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 587-04
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
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119
                 122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                                                                                                                143;
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                                                              64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDENVLVTCNRPEQEIRTIKFQEFS 118
                                                                                        62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLLTCDRPDLDLRFTIKFQEYS 121
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PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                 PGORWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beckmann, M.
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                                                                                                                                                                                                               25.4%; Score 623; DB 1
39.2%; Pred. No. 1e-44;
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                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                               DB 1; Length 346;
                                                                                                                                                                                                   116;
                                                                                                                                                                                                   Indels
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APPLICANT: Lyman, I
APPLICANT: Beckmann
APPLICANT: Baum, P
                                                                 Matches 143;
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5627267
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 01-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUWBER: 32,172
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOPTWARE: Microsoft Word for Apple,
                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                              LENGTH:
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                              PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08458077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---
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PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                               346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                 (206) 233-0644
                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baum, Peter R
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                                                                                25.4%;
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o. 5627267el Cytokine Designated elk Ligand
                                                               48; Mismatches 116;
                                                                                                                                                                                                                                                                                                   2807-A
                                                                                Score 623; DB 1
Pred. No. 1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version
                                                                                              DB 1;
                                                                                               Length 346;
                                                                 Indels
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                                                                 58;
                                                                 Gaps
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; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-460-741-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Appirous Sequence 2, Appirous 5670625
                                                                                                        TELEFAX: (206) 233-06
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Lyman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
COMPUTER READABLE FORM:
TYPE: Ploppy disk
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acid
TYPE: amino acid
                                                                                                                                                     NAME: Seese, Kathryn A.
REGISHON NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 280
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baum, Peter R
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
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                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                               ELECUTE: (200)
TELEPHONE: (206)
                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/460,741 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                 d: 346 amino acids
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Baum, Peter 1
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                                    linear
                                                                                                                                     (206) 587-0430
                  protein
                                                                                                                      233-0644
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RESULT 13
US-08-747-240-2
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Best Local Similarity
Matches 143; Conserv
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                                                                                                                                                                     JOSEPH APPLICATION. Apple System 7.1

GURRENT APPLICATION DATA:

APPLICATION NUMBER: US/8/747,240

FILING DATE: 12-NOV-1996

CLASSIFICATION: 435

PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 288
TELECOMMUNICATION INFORMATION:
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 5728813el
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII
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                                                                                                                                                                                                                                                                                                                                                                                           Washington
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Beckmann, M. Patricia
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Carpenter, Me
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                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melissa
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                      2807-A
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                                                                                                                                                                                                                                                                        Version 5.1a
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US-08-299-567-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08299567 Patent No. 5747033
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Davis,
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/299
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                            ZIP: 10591-6707

ZIP: 10591-6707

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                            STREET: 777 Old CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII
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777 Old Saw Mill River Road
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APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa K.
TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
FILE REFERENCE: GENENT.67CPV3
CURRENT APPLICATION NUMBER: US/09/039,642B
CURRENT FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 09/213,403
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR APPLICATION NUMBER: 08/47,240
PRIOR APPLICATION NUMBER: 08/47,240
PRIOR APPLICATION NUMBER: 08/460,741
                                ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-039-642B-2
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US-09-039-642B-2
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US-08-299-567-6
                                                                                     NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09039642B Patent No. 6540992
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity 39.2%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acid
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TOPOLOGY: unknown
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                                                           STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
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48; Mismatches 116;
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Search completed: December 21, 2005, 14:37:38 Job time : 38.2013 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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US-10-0298-907-16
US-10-698-907-16
US-10-698-907-8
US-10-698-907-7
US-10-698-907-7
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US-10-698-907-14
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US-10-698-907-14
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US-10-138-787-4
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g &	Query Ma Best Loo Matches	RESULT: US-10-0: Seque: Seque: Publi: GENI INF		20 20 20 20 20 20 20 20 20 20 20 20 20 2
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PHS	ilarity Conserva	-121-2 e 2, Application US/10021121 tion No. US20020142444A1 AL INFORMATION: APPLICANT: Caras, Ingrid W TITLE OF INVENTION: A2-1 Neur NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, In STREET: 1 DNA Way CITY: South San Francisc STATE: California COUNTRY: USA ZIP: 94080 COMPUTER READABLE FORM: COUNTRY: USA ZIP: 94080 COMPUTER: HEADABLE FORM: COUNTRY: USA ZIP: 94080 COMPUTER: HEADABLE FORM: COUNTRY: USA ZIP: 94080 COMPUTER: HIM PC compati OPERATING SYSTEM: PC-DOS SOFTWARE: Winpatin (Gene CURRENT APPLICATION NUMBER: US/1 FILING DATE: 19-Mar-1996 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: US/1 REFERENCE/FOCKET NUMBER: 15-Mar-1996 ATTORNEY/AGENT INFORMATION REGISTRATION NUMBER: 36-74 TELEPHONE: 650/25-8674 TELECOMMUNICATION THORMATION TELEPHONE: 650/25-8674 TELECOMMUNICATION SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE DESCRIPTION: SEQ ID -121-2		18.4 18.4 18.2 18.0 19.0 11.6 11.6 11.6 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8
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PHSGPGGVRVGALLILGVLGLVSGLSLEÞVYMNSANKRFQAEGGYVLYPQIGDRLDL 	Score 2450; Pred. No. 1. 0; Mismatches	rotr nc. co co co co syms syms syms syms syms syms syms sym	ALIGNMENTS	US-10-800-350-390 US-10-698-907-20 US-10-698-907-21 US-10-800-350-388 US-10-800-077-888 US-90-864-761-4826: US-90-864-761-4826: US-90-862-179A-15 US-11-097-143-255-27-13 US-11-097-143-2343) US-90-862-179A-16 US-10-138-787-12 US-10-138-787-12 US-10-138-787-12 US-09-904-954-2 US-09-904-954-2 US-09-733-756-2 US-10-241-220-72
JEPVYWNSANK JEPVYWNSANK	0; DB 4; 1.6e-179; hes 0;	ophic Factor Mb floppy disk -DOS ch) 21,121 21,121 y E. 001	TS	350-390 307-29 307-21 307-21 350-388 350-388 377-388 377-388 377-62 357-62 354-2 354-2 354-2 354-2
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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-021-121-4
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US-10-021-121-4
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                                                                                                                                APPLICATION UNMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/08/635,130
FILING DATE: 19-Max-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOrchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 191001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEPAX: 650/95-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Query Match
Best Local Similarity
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ADDRESSEE: Genente
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APPLICANT: Caras, Ingrid W
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                                                                                      TYPE: Amino Acid TOPOLOGY: Linear
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STATE: California
COUNTRY: USA
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                                                                                                                     LENGTH: 340 amino acids
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75.1%;
100.0%;
Score 1841; DB 4;
Pred. No. 6.4e-133;
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                   Length 340
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Best Local Simi
Matches 338;
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SEQ ID NO 4256
LENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION UNMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
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ORGANISM: Homo
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                         GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
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RESULT 5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-907-16
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CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2002-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEO ID NOS: 25
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Sequence 3, Application US/10138787
Publication No. US20020172984A1
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.1%; Score 1841; DB 5; Length 340; Best Local Similarity 100.0%; Pred. No. 6.4e-133; Matches 338; Conservative 0; Mismatches 0; Indels
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APPLICANT: Holmberg, Johan
TITLE OF INVENTION: Use of Ephrins and Related Molecules
TITLE OF INVENTION: Proliferation
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CURRENT APPLICATION NUMBER: US/10/417,924A
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: 09/051,994
PRIOR FILING DATE: 1998-04-24
PRIOR PELLING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 0CT/US96/17201
PRIOR APPLICATION NUMBER: 6C/007,015
PRIOR PILING DATE: 1996-10-25
PRIOR APPLICATION NUMBER: 6C/007,015
PRIOR PILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 2
LENGTH: 340
TYPER: DET
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US-10-417-924A-2
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 340
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Best Local (
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TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH
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PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR EILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
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CURRENT FILING DATE: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: REG-341Z
                FEATURE:
NAME/KEY: Misc. feature
LOCATION: (166)
                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa = unknown or other
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Pred. No. 1.3e-132;
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APPLICANT: Fisen, Jonas
APPLICANT: Holmberg, Johan
ITITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
ITITLE OF INVENTION: Proliferation
FILE REFERENCE: 21882-529 UTIL
CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT APPLICATION NUMBER: US 60/460,488
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2003-04-03
PRIOR FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2002-11-09
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
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US-10-698-907-8
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Best Local Similarity 99.7%;
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Best Local Similarity 95.6%;
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Pred. No. 1.5e-127;
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Pred. No. 1.8e-132;
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                                                   Sequence 7, Application US/10698907
Publication No. US20050049194A1
GENERAL INFORMATION:
 APPLICANT: Frisen, Jonas
APPLICANT: Holmberg, Jo
TITLE OF INVENTION: Use
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APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gleon, Gary M.
APPLICANT: Gleon, Gary M.
APPLICANT: Gleon, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEON
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-408-765A-2695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 283; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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241
                                            296
                                                                                                                                                                                                                                                                                                                                   116 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                           56 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 115
                                  ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                                                                                                                                                                                                                                VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
                                                                                                                                                                                                                                                                                       KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA
                                                                                                                                                                                                                                                                                                                                                                                    DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY
                                                                                           ALLLIGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI
                                                                                                                                       ALLLIGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGI
                                                                                                                                                                                           VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.3%; Score 1550; DB 4; ilarity 100.0%; Pred. No. 1.1e-110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338
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Johan

Ephrins

and Related Molecules

to Regulate

Cellular

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RESULT 10
US-10-021-121-9
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CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT FILLING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2002-21-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR APPLICATION NUMBER: US 60/345,206
PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/10021121
Publication No. US20020142444A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.7%; Score 628.5; DB 5; Best Local Similarity 41.8%; Pred. No. 7.3e-40; Matches 137; Conservative 49; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF INVENTION:
                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEKVSGDYGHPYYIVQDGPPQSPPNIYY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLLMVLCRTAISRSIVLEPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TÄDSVFCPH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
APPLICATION NUMBER: US/10/021,121 FILING DATE: 06-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEKVSGDYGHPVYIVQEMPPQSPANIYY 334
                                                                                                                                                                                              ZIP: 94080
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                     USA
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             APPLICANT: CARPENTER, Melissa K.
TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELF
FILE REFERENCE: GENENT: 67CPDV3
CURRENT APPLICATION NUMBER: US/10/356,289
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US/99/039,642B
PRIOR FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 08/213,403
PRIOR FILING DATE: 1994-03-15
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR APPLICATION NUMBER: 08/747,240
PRIOR FILING DATE: 1996-10-12
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                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10356289
Publication No. US20040022767A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
    APPLICATION NUMBER: 08/460,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340
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                                                                                                                                                                                                                                                                                                        Baum, Peter R
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REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Max-1996
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phb., Timothy E.
REGISTRATION NUMBER: 36,700
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CPRARPPGPHSSPNYBFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
                                  ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                  GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                                                                                                                                                                        SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD
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                                                                                                                                                                                                                                                                                                                                                              PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT
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                                                                                                                                                                             -----LLLLGVAGAGGA------MCWRRRRAKPSESRHPGPGSFGRGGSLGL
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39.2%; Pred. No. 2e-39;
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Sequence 60, Application US/10712124

Publication No. US20040146907A1

GENERAL INFORMATION:
APPLICANT: SMITH, VICTORIA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
FILE REFERENCE: P2000R1

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US/10/712,124

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US 60/425,813

PRIOR APPLICATION NUMBER: US 60/425,813

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 123

SEQ ID NO 60

LENGTH: 346

TYPE: PRI
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US-10-712-124-60
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US-10-356-289-2
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows
SEQ ID NO 2
                                                                                                              Query Match 25.4
Best Local Similarity 39.3
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 143;
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TYPE: PRT
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               CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRPTIKFQEYS 121
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                                                      PNIYY 338
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 CPRAEAGRP---
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                                                                                                             25.4%; Score 623; DB 4; Length 346
39.2%; Pred. No. 2e-39;
tive 48; Mismatches 116; Indels
-YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
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Best Local Similarity
Matches 143; Conserv
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APPLICANT: Ng, Dean
APPLICANT: Ng, Dean
TITLE OF INVENTION: DIAGNOSTIC METHODS FOR CANCER DETECTION
FILE REFERENCE: 5.189-2
CURRENT APPLICATION NUMBER: US/10/789,378
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: 10/441925
PRIOR FILING DATE: 2003-05-19
PRIOR FILING DATE: 2003-05-17
PRIOR APPLICATION NUMBER: 60/381619
PRIOR APPLICATION NUMBER: 60/450886
PRIOR APPLICATION NUMBER: 60/450886
PRIOR FILING DATE: 2003-02-26
NUMBER OF SEQ ID NOS: 131
SEQ ID NO 30
LENGTH: 346
TYDE: PRT
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                                           -----LLLLGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL
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vo. US20050003390A1
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    -RAAALSL
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RESULT 15
US-09-754-105-2
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PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/345,206
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Holmberg, Johan
TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
TITLE OF INVENTION: Proliferation
FILE REFERENCE: 21882-529 UTIL
CURRENT APPLICATION NUMBER: US/10/698,907
CURRENT FILING DATE: 2003-10-31
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NUMBER OF SEQ ID NOS: 25
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APPLICANT: Holmberg, Jo
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ORGANISM: Homo sapiens
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Application US/09754105

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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-754-105-2
Search completed: December 21, 2005, 14:41:50 Job time : 130.201 secs
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CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: 09/329,531
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cerretti, Douglas
APPLICANT: Reddy, Pranhitha
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED
FILE REFERENCE: 28232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 25.3%; Score 620.5; DB 3; Local Similarity 40.5%; Pred. No. 3e-39;
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                                                                                               YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
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GO; GO:0005807; C:integral to plasma membrane; TAS.
GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
InterPro; IPR001799; Ephrin.
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EMBL; U66406; AACS1203.1; -; mRNA.

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-!-FUNCTION: May play a pivotal role in forebrain function.
-!- grinction: May play a role in constraining the orientation of vitro. May play a role in constraining the orientation of longitudinally projecting axons (By similarity).
-!- SUBCILIULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Highly expressed in brain; expressed embryonic floor plate, roof plate and hindbrain segments.
-!- SIMILARITY: Belongs to the ephrin family.
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PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
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INTERACTIONS WITH GRIP1 AND GRIP2.
INTERACTIONS WITH GRIP1 AND GRIP2.
TISSUE=Fetal brain;
MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
MEDLINE=99211380; PubMed=10197531; Scheiffele P., Herb A., Seeburg P.H.
SEQUENCE
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PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
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TRANSMEM
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ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse as long as its content is in no way modified and this s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Transmembrane SIGNAL 1 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI; MGI:109196; Efnb3.
GO; GO:0005615; C:extracellular space; TAS
GO; GO:0016021; C:integral to membrane; TAS
GO; GO:0007628; P:adult walking behavior;
GO; GO:0016198; P:axon choice point recogn
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the orientation of longitudinally projecting axons.";

Development 127:1397-1410(2000)
                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00812; Ephrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20171264; PubMed=10704386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vitro. May play a role in constraining the orientation of longitudinally projecting axons.

SUBUNIT: Interacts with GRIP1 and GRIP2 (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed on lateral floor plate cells, specifically on commissural axon segments that have passed through the floor plate. Expressed in cells of the retinal ganglion cell layer during retinal axon guidance to the optic disk.

DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the period of commissural axon pathfinding.

SIMILARITY: Belongs to the ephrin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: May play a pivotal role in forebrain function. Binds and induce the collapse of, commissural axons/growth cones in
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BC052001; AAH52001.1; -; mRNA.
BC058617; AAH58617.1; -; mRNA.
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                                                                                                                                                                                                                                                        Similarity
SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
                                                                                     LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                                                          MGPPHSGPGGVRVGALLLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                 LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                                  MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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95.6%;
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                                                                                                                                                                                                                                                                                                                     ME.
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

PDZ recognition motif (Poter N-linked (GLONAC...) (Poter By similarity.

By similarity.
                                                                                                                                                                                                                              Score 1771; D
Pred. No. 3.4e
7; Mismatches
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Barzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266; Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobor Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Ephrin B3 (16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130040B01 product:m-ephrin-B3).
Name=Efnb3; ORFNames=RP23-56I20.5-001;
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Head;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                 "Functional annotation of Nature 409:685-690(2001).
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Euarchontoglires; Glires;
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lires; Rodentia; Sciurogna
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                                        Gojobori
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RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothai C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothai C., Corbani L.E., Cousins S.,
RA Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Ponttus J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdala R.D., Tomita M.,
RA Vuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Wilming L.G., Wynshaw-Boris A., Yanagiswa M., Yang I., Yang I.,
RA Wilming L.G., Wynshaw-Boris A., Yanagiswa M., Yang I.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Nayashizaki V., Sasaki D., Shibata K., Shinagawa A.,
Nayashizaki V., Watarshion R., Lander E.S., Rogers J.,
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Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
L Submitted (JUL-2001) to the EMBL/Genjank/DDBJ databases.
EMBL; AK048305; BAC3329-1; -; MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/63; TISSUE-Head;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
Bequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUE-Head;
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Nature 420:563-573(2002).
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    323;
                                               Similarity
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                                               72.3%;
                                               Score 1771;
Pred. No. 3
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        Mismatches
                                                    .4e-106;
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        8,
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        Indels
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                                                                                                                                                                                                                                                                                                                                             MEDIINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281; Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B., Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.; "Morphogenesis of prechorial plate and notochord requires intact eph/ephrin b signaling."; Dev. Biol. 234:470-482(2001).

EMBL, AF375227; AAK64277.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
01-OCT-2003
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Q90Z31;
                                                                                                                                                                                                                            PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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Ensembl; ENSDARG00000008177; Danio rerio
                                                                                                                                                                                                                                                                    Pfam; PF00812; Ephrin;
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                                                                                                                                                                                                                                                                               InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRARE
                                                                                                                                                                                                                                                                                             N; ZDB-GENE-010618-3; efnb3.
GO:0016020; C:membrane; IEA.
                         129
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           FRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME
                                                                PHSSPNYEFYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE
                                                                                                        GLGILLIFLVDLLG-ITATNWEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG
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FKTNHDYF11ATSDGTRQGLESMRGGVCATQGMKVVLKVGQSPYGLPAKSPKPDS
                                                   PRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE
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                                                                                                                                                                        Score 914; DB 2;
Pred. No. 5.4e-51;
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                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Klausherg R.L., Feingold E.A., Grouse L.H., Darge J.G.,
RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Tand mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 188; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ULT 5
203 BRARE
050203 BRARE PRELIMINARY;
050203;
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases EMBL; BC095605; AAH95605.1; -; mRNA. SEQUENCE 342 AA; 36885 MW; 1629532234F85386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Efnb3 protein.
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13-SEP-2005 (TrEMBLrel.
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FRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME
                                                                                                                                                                                                                                                                                                        GVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIPLR---TSDSAYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 329
                                                                                                                PRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE
                                                                                                                                                          PHSSPNYEFYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE
                                                                                                                                                                                                                                                           GLGILLIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                               37.3%; Score 914; DB
54.5%; Pred. No. 5.6e
cive 43; Mismatches

    Created)
    Last sequence update)
    Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                      74;
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Matches
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Best Local
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SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00812; Ephrin.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
Prodom; PS00687; ALDEHYDE DEHYDR_GLU;
PRODOM; PS00687; ALDEHYDE DEHYDR_GLU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUCLEMATION: head;
TISSUB=Embryonic head;
MEDLINE=20099673; PubMed=10633856;
MEDLINE=20099673; PubMed=10633856;
DOI=10.1002/(SICI)1997-0177(199912)216:4/5<361::AID-DVDY5>3.0.CO;2-W;
DOI=10.1002/(SICI)1997-0177(199912)216:4/5<361::AID-DVDY5>3.0.CO;2-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9PT69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ236866; CAB65511.1; -; mRNA.
HSSP; P52800; 11KO.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002086; Aldehyd_dehydrog
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helbling P.M., Saulnier D.M.E., Robinson Wilkinson D.G., Brandli A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephrin-B3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Comparative analysis of embryonic gene expression defines potential interaction sites for Xenopus EphB4 receptors with ephrin-B ligands."; eev. Dyn. 216:361-373(1999).
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XENLA
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HPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPV
                                                                            LPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESR
                                                                                                                                                             TREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSL-EPGKEN
                                                                                                                                                                                                     GTKEEMSSCSILRTPNLLLTCDRPSQDLRFTIKFQEFSPNLWGHEFQSQRDYYIIATSDG
                                                                                                                                                                                                                           GGAQG-RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG
                                                                                                                                                                                                                                                                                  ISALSIDPIYWNSSNKRFEDTEGYVLYPQIGDRIDLICPRSEPQGPFSSSPYEYYKLYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY
                                        V-GETSGNATKTGENGPLPISHVPLVAGAAGGAALLLL-VFGVVGWVCHRRRQAKHSDTR
                                                                                                                       TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVPNPDIPN
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
35913 MW;
                                                                                                                                                                                                                                                                                                                                                                                        37.1%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                      Score 910; DB 2;
Pred. No. 9.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
; 4BB0FA39D4C22DCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
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; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                     Gaps
    322
                                                                                262
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                                                                   RX MEDILINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schein, J.R., Jones S. J. M. Mayra M. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jenkins N.A., "Isolation of kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS2800;
01-OCT-1996 (Rel. 34, Created,
01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand
Ephrin-B2 (HTK ligand) (HTK-L) (ELF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95199254; PubMed=7534404;
Bennett B.D., Zeigler F.C., Gu Q.,
Gillett N., Matthews W.;
"Molecular cloning of a ligand for
tyrosine kinase Htk.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P52800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5; Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P., Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J., Jenkins N.A., Fletcher R.A.;
                             Schnerch A., Schein J.E., Jones S.J.M., Marra M.A. "Generation and initial analysis of more than 15,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6;
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STRAIN=ICR; TISSUE=E
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STRAIN=CB57BL/6J X (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in mouse embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32:1197-1205(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=7651410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A. 92:1866-1870(1995).
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                                   full-length human
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the orientation of longitudinally projecting axons.";

Development 127:1397-1410(2000)
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Henkemeyer M., Nikolov D.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
PubMed=11780069; DOI=10.1038/414933a;
Himanen J.-P., Rajashankar K.R., Lackr
                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                         removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed on lateral floor plate cells, specifically on commissural axon segments that have passed throuthe floor plate. Expressed in cells of the retinal ganglion cell layer during retinal axon guidance to the optic disk.

DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
                                                                                                                                                                                                                                                                                                                                                                                                                               period of commissural axon pathfinding. PTM: Inducible phosphorylation of tyrosine residues in cytoplasmic domain (By similarity). SIMILARITY: Belongs to the ephrin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor tyrosine kinase EPHB4.
SUBCELLULAR LOCATION: Type I membrane
                                                                                                                                                                                                                                                                                                                                                                    as long as
                                                                                                                                                                                                                                                                                                                                                                                 European
                                                                                                                                                                                                                                                                                                                                                                               Swiss-Prot entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
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MGI; MGI:105097; Efnb2.

GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0015886; C:plasma membrane; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005915; P:lymph vessel development;
GO; GO:0001945; P:lymph vessel development;
GO; GO:0001945; P:organogenesis; IMP.
InterPro; IPR001799; Ephrin. CHAIN
TOPO DOM
TRANSMEM
TOPO DOM
MOTIF PDB; 1IKO; X-ray; P=30-207. PDB; 1KGY; X-ray; E/F/G/H=31-168. Ensembl; ENSMUSG00000001300; Mus SIGNAL PROSITE; PS01299; EPHRIN; 1. Neurogenesis; D-structure; I49766; U16819; AAA99708.1; -; mRNA. L38847; AAAC42052.1; -; mRNA. U30244; AAA82934.1; -; mRNA. BC057009; AAH57009.1; -; mRN PF00812; Ephrin; 1 S; PR01347; EPHRIN. 1 29 233 254 334 I49766 Phosphorylation; Signal 336 232 253 336 336 -; mRNA Potential.
Cytoplasmic (Potential)
PDZ recognition motif (Extracellular (Potential). Potential Signal; musculus. Differentiation; Glycoprotein Transmembrane. (Potential)

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                              UMIT 8
UM3_MOUSE
Q4FUM3_MOUSE PRELIMINARY;
Q4FUM3,
Q4FUM3,
13-SEP-2005 (TrEMBLrel. 31, 1)
13-SEP-2005 (TrEMBLrel. 31, 1)
13-SEP-2005 (TrEMBLrel. 31, 1)
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CARBOHYD
CARBOHYD
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CARD
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Name=Efnb2;
Mus musculus (Mouse)
Eukaryota; Metazoa;
                       Efnb2 protein.
                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                           GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                              GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                        PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
                                                                                                                                              WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                            GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                          GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK
                                                                                                                                                                                                                                                        GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                  YEKVSGDYGHPVYIVQEMPPQSPANIYY
                                                                                                            YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                                                                                                                               KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
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                                                                                                                                                                                                                                                                                      Conservative
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                               Created)
Last sequence update)
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Pred. No. 1.4
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N-linked
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A -> T (in Ref. 1).
  Craniata; Vertebrata; Euteleostomi;
                                                             PRT;
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Best Local S
Matches 137
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01-OCT-1996
01-OCT-1996
                                                                                                                                  MEDLINE-9439923; PubMed-8070404;
Beckmann M.P., Cerretti D.P., Baum P., Vand Farrah T., Kozlosky C., Hollingsworth T., Serletcher F.A., Lhotak V., Pawson T., Lyman "Molecular characterization of a family of tyrosine kinase receptors.";
EMBO J. 13:3757-3762(1994).
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MEDLINE=95063919; PubMed=7973638;
Davis S., Gale N.W., Aldrich T.H., Maisonpierre
Pawson T., Goldfarb M., Yancopoulos G.D.;
"Ligands for EPH-related receptor tyrosine kinas
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Muroidea; Muridae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ephrin-B1 precursor (EPH-related receptor tyrosine (LERK-2) (ELK ligand) (ELK-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=EFNB1; Synonyms=EFL-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
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                                          PubMed=7973638;
W., Aldrich T.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homin
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Pred. No. 1.4
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Mismatches 129;
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                                               P.C., Lhotak
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
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RA Cree A., Gunaratine P., Havlak P., Hodgson A., Metzker N.L.,
RR Richards S., Scott G., Steffen D., Sodergren E., Meeler D.A.,
RR Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Barerjee R.
RA Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Barerjee R.
RA Barker G.E., Barlow K.F., Barrett I.P., Bares K.N., Barer D.M.,
RA Beasley H., Beasley O., Beck A., Bethel G., Blachschmidt K., Brady N.,
RA Button J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
Corby N., Connor R.E., David R., Davies J., Duhh H., Dodsworth S.,
RA Circy D., Connor R.E., David R., Davies J., Duhh H., Dodsworth S.,
RA Circy N., Connor R.E., David R., Davies J., Duhh H., Dodsworth S.,
RA Circy N., Connor R.E., David R., Davies J., Duhh H., Dodsworth S.,
RA Circy N., Connor R.E., David R., Davies J., Duhh H., Dodsworth S.,
RA Circy N., Connor R.E., David R., Davies J., Duhh H., Dodsworth S.,
RA Circy N., Connor R.E., David R., Dunn M., Durbin K.J., Dutta I.,
RA Cades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
RA Faulkner L., Francis F., Frankland J., Fraser A.E., Galgoczy P.,
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA Hunt P.J., Hunt A.R., Isherwood J., Jocob L., Johnson D., Jones S.,
RA Gilbert J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA Kioschis P., Klages S., Kights A.J., Kosiura A., Kovar-Smith C.,
RA Gillow P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA Milne S., Miner G., Misty S.L., Morgan M., Hewis L. Liu W.,
RA Laird G.K., Langford C., Lawlor S., Heversha M., Lewis L. Liu W.,
RA Laird G.K., Langford C., Lawlor S., Methari A., Kovar-Smith C.,
RA Milne S., Miner G., Misty S.L., Morgan M., Metthews L.H.,
RA Milne S., Miner G., Misty S.L., Morgan M., Metthews L.H.,
RA Giller F., K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA Milne S., Fatel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA Raider K., Schlessinger D.,
                                                                                                                                             Wilson R.K., Watter
Wilson D.L., Weinstock G., -
Nelson D.L., Weinstock G., -
Nelson R.A., Beck S., Rogers J., Be
The R.A., Beck S., Rogers J., Be
The R.A., Beck S., Rogers J., Be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A., Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R. Jones M.C., Hurles M.E., Andrews T.D., Scott C.E., Searle S. Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E.,
                           NUCLEOTIDE SEQUENCE
TISSUE=Eye, and Skir
MEDLINE=22388257; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15772651; DOI=10.1038/nature03440;
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266:816-819(1994).
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R.L.,
                                                                                                                                                                                                                                                            Weinstock G., Sulston J.E.,
                                                              Skin;
Feingold
                           PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                [LARGE
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E.A.,
                                                                                                SCALE MRNA].
                                                                                                                                                                                                     Bentley D.R.;
Grouse L.H., Derge J.G.,
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Hubbard T.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Scheetz M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Chnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Touchman J.W., Green E.D., Dickson M.C., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Touchman J.W., Green E.D., Dickson M.C., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Touchman J.W., Green E.D., Dickson M.C., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Touchman J.W., Green E.D., Dickson M.C., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Touchman J.W., Green E.D., Dickson M.C., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Touchman J.W., Green E.D., Marra M.A.;
  VARIANTS CFNS ARG-27; LEU-54; SER-119; HIS-119; ALA-137; PHE-1 SER-151; SER-153; TYR-153 AND ARG-182.

PubMed=15959873; DOI=10.1002/humu.20193;

Wieland I., Reardon W., Jakubiczka S., Franco B., Kress W., Vincent-Delorme C., Thierry P., Edwards M., Koenig R., Rusu C. Schweiger S., Thompson E., Tinschert S., Stewart F., Wieacker "Twenty-six novel EFNB1 mutations in familial and sporadic craniofrontonasal syndrome (CFNS).";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Twigg S.R.F., Kan R., Babbs C., Bochukova E.G., Robe Wall S.A., Morriss-Ray G.M., Wilkie A.O.M.; mutations of ephrin-B1 (EFNB1), a marker of tissue formation, cause craniofrontonasal syndrome."; proc. Natl. Acad. Sci. U.S.A. 101:8652-8657(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15124102; DOI=10.1086/421532; Wieland I., Jakubiczka S., Muschke P., Gerlach K.L., Adams R.H., Wiescker P.; "Mutations of the ephrin-Bl gene cause Am. J. Hum. Genet. 74:1209-1215(2004).
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[8]
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MEDLINE=99211388;
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                                                                                                        FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and Binds to, and induce the collapse of commissural axons/grocomes in vitro. May play a role in constraining the orienta longitudinally projecting axons (By similarity). SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Heart, placenta, lung, liver, skeletal
cytoplasmic
DISEASE: Def
                                                                kidney, pancreas
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Inducible phosphorylation of plasmic domain (By similarity) ASE: Defects in EFNB1 are a ca
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AND VARIANT HIS-15
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Best Local S
Matches 143
                                                                                                        EFNB2 HUMAN STANDARD; PRT; 333 AA P52795; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update Ephrin-B2 precursor (EPH-related receptor t (LERK-5) (HTK ligand) (HTK-1) (HTK-1) (HERK-5) (HTK ligand) (HTK-1) (HTK
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EMBL; L37361; AAA52369.1; -; mRNA.
EMBL; U09303; AAB4112.7; -; GENOMIC_DNA.
EMBL; AL136092; CAB86409.1; -; GENOMIC_DNA.
EMBL; BC01649; AAH16649.1; -; mRNA.
EMBL; BC052979; AAH52979.1; -; mRNA.
                      Eukaryota; Metazoa;
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Name=EFNB2; Synonyme=EPLG5, H
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ween the Swiss Institute of Bioinformatics and the El
European Bioinformatics Institute. There are no rest
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SIMILARITY: Belongs to the ephrin family.
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Jordan H., Moore T. Max S.I., wang J., Hsteh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Botal G.M., Ugdin T.B., Toshiyuki S., Carrinci P., Prange C., RA Bownstein M.J., Ugdin T.B., Toshiyuki S., Carrinci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RRA Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Ra Radriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.; Skalska U., Smailus D.E., RA Rodriguez CDNA sequences.";

PRI "Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences.";

PRI "Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences.";

PRI "Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences.";

PRI "Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences.";

PRI "Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences.";

PRI "Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences.";

PRI "Generation
  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           increased tumorigenicity and metastatic potential melanomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95199254; PubMed=7534404; Bennett B.D., Zeigler F.C., Gu Q., Gillett N., Matthews W.; "Molecular cloning of a ligand for tyrosine kinase Htk.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-9819220; PubMed-9533549;
Vogt T., Stolz W., Welsh J., Jung B.,
Landthaler M., McClelland M.;
"Overexpression of Lerk-5/Eplg5 messe:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5; Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P., Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J., Jenkins N.A., Fletcher R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jenkins N.A., Fletcher R.A.; "Isolation of the eph-related receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                            removed.
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                                                                                                                                                                                              SIMILARITY: Belongs to the ephrin family.
                                                                                                               Swiss-Prot entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
U16797;
L38734;
U81262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer Res. 4:791-797(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acad. Sci. U.S.A. 92:1866-1870(1995)
AAA99707.1;
AAC41752.1;
AAD03786.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32:1197-1205(1995).
    1.1.1
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  mRNA.
mRNA.
mRNA.
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Best Local S
Matches 133
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                                      OSTV56 HUMAN PRELIMINARY;
OSJV56;
10-MAY-2005 (TrEMBLrel. 30, 0
10-MAY-2005 (TrEMBLrel. 30, 1
10-MAY-2005 (TrEMBLrel. 30, 1
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CARBOHYD
DISULFID
DISULFID
SEQUENCE
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HGNC; HGN
MIM; 6005
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                    Ephrin-B2 (Fragment).
Name=EFNB2; ORFNames=RP11-272L14.1-001;
  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
           Homo sapiens (Human)
                                                                                          11
HUMAN
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GO:0046875; F:ephrin receptor binding; TAS.
GO:0007267; P:cell-cell signaling; TAS.
GO:0009653; P:morphogenesis; TAS.
cerPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                               134
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                                                                                                                                                                           251
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                               WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                              DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                    GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK
                                                                                                                                                                                                                                                                                                                  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                            GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                                                        GALLLIGVIGIVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                    YEKVSGDYGHPVYIVQEMPPQSPANIYY
                                                                                                                                                       YEKVSGDYGHPVYIVQDGPPQSPPNIYY
                                                                                                                                                                           KYRRRHRKHSPOHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                                                                                                    GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFÄGIÄSGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                       GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                                                           DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
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230
251
251
331
36
139
62
89
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                            36923
                                                                                                                                                                                                                                                                                                                                                                                             25.3%;
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                                        Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.

Cytoplasmic (Potential).

PDZ recognition motif (Potential).

N-linked (GlcNAc...) (Potential).

N-linked (GlcNAc...) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephrin-B2.
Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
  Craniata;
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mRNA.
mRNA.
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            6D9932A632626AEA CRC64;
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                                                                                                                                    331
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                                                                                                                                                                                                                                                                                                                                                                                             5; DB 1;
4.4e-32;
  Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Neurogenesis;
                                                                                  ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential).
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  Euteleostomi;
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PRESULATION OF THE CASE OF THE
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Best Local S
Matches 133
                                                                                                                                                                                                                                                   Menzel P., Pasquale E.B.;
"Coding sequence of chicken epi
submitted (AUG-1999) to the EMI
EMBL; AF180729; AAD53948.1; -;
HSSP; P52800; 11KO.
SWR; OSPUJ4; 29-169.
SWR; OSPUJ4; 29-169.
GO; GO:0016020; C:membrane; IEJ
InterPro; IPR001799; Ephrin.
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Submitted (MAY-2005) to the EMBL/Genually, Luca Submitted (MAY-2005) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002
Ephrin-B2 precursor.
Ephrin-B2 precursor.
Gallus gallus (Chicken).
               CHAIN
SEQUENCE
                                                                  ProDom; PD00253; Ephrin;
PROSITE; PS01299; EPHRIN;
Signal.
SIGNAL 1 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PUJ4 CHICK PRELIMINARY;
Q9PUJ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                Pfam; PF00812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
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CHICK
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                                                                                                                                                                                                                                Ephrin;
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IEA.
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EMBL/GenBank/DDBJ
-; mRNA.
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Last
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Pred. No. 4.4e-32;
                  ephrin-B2.
; 4C28E8CB211B7783
                                                                           Potential.
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; Galliformes; Phasianidae; Phasiani
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                      CRC64;
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Best Local Similarity
Matches 133; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHICK
EFNB1 CI
073612;
                    Pfam, PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97223524; PubMed=9070326; DOI=10.1006/dbio.1996.8496; Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M., Pasquale "Reciprocal expression of the Eph receptor Cek5 and its ligand(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
Ephrin-Bl precursor (CEKS ligand) (CEL5-L).
peveropmental protein; Phosphorylation; Signal
                                                                                                           EMBL; U72394; AAC07986.1; -;
HSSP; P52800; 1IKO.
InterPro; IPR001799; Ephrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves;
                                                                                                                                                                                                                                                                                    SUBUNIT: Binds to the receptor tyrosine kin with GRIP1 and GRIP2 (By similarity).

SUBCELLULAR LOCATION: Type I membrane prote PYM: Inducible phosphorylation of tyrosine cytoplasmic domain (By similarity).

SIMILARITY: Belongs to the ephrin family.
                                                                                                                                                                                                                 s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                   early retina.";
. Biol. 182:256-
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       Signal;
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Pred. No. 4.4e
52; Mismatches
                                                                                                                                                  mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
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(CEL5-L).
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No. 4.4e-32;
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                        Neurogenesis;
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Matches 144
                                                                                                           Durbin L., Brenz
Shanmugalingam S
"Eph signaling i
NUCLEOTIDE SEQUENCE.

MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
Chan J., Mabby J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.!
"Morphogenesis of prechordal plate and notochord requires inta
eph/ephrin b signaling.";
                                                                                                  "Eph signal somites.";
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SEQUENCE
                                                                                                                                                                                  Ephrin-B2a precursor.

Name=efnb2a; Synonyms=efnb2;

Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio rerio (Zebrafish) (Caniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform

Cyprinidae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
10-MAY-2005 (Rel. 47, Last ann
                                                                                                                                                                                                                                                                                                               EFNB2 BRARE
073874;
                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=98438455; PubMed=9765210;
Durbin L., Brennan C., Shiomi K.,
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n S., Guthrie I
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Potential.

Cytoplasmic (Potential).

PDZ recognition motif (Potential).

N-linked (GlCNAc. . .) (Potential).

By similarity.

By similarity.
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Pred. No. 5.
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Ephrin-B1.
                                                                                                            K., Cooke J.,
  Lindberg R.,
  segmentation
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and differentiation
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RESULT 15
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ID Q90Z33_B;
AC Q90Z33;
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PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ004863; CAA06168.1; -; EMBL; AF375225; AAK64275.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00812; Ephrin; 1
PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZFIN; ZDB-GENE-990415-67; efnb2a.
GO; GO:0008039; P:synaptic target recognition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSDARG00000020164; Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytoplasmic domain (By similarity).
SIMILARITY: Belongs to the ephrin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. 234:470-482(2001)
SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: Inducible phosphorylation of tyrosine residues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
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                                                                                            LRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY
                                                                                                                                            AGAGGAMCWRRRRAKPSESRHPGPGSFG-----RGGSLGLGGGGGMGPREAEPGELGIA
                                                                                                                                                                                                                                      DYYIIATSDGTREGLESLOGGYCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA
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                                                                       LR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY
                                                                                                                    VFL--LLKYRRHRKHS-PQHATTLSLSTLATPKRGGS---
                                                                                                                                                                   KDSKSNEVLKPDASPHGEDK--GDGNKSSSVIGSEVAL----FACIASASVIVIIIIIML
                                                                                                                                                                                           AHS----LEP----
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             PRELIMINARY;
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Cytoplasmic (Potential).
PDZ recognition motif (Po
N-linked (GlcNAc...) (P
N-linked (GlcNAc...) (P
N-linked (GlcNAc...) (P
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4; Mismatches
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Ву
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Extracellular (Potential).
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              PRT;
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/ similarity.
189ED82372C71C8B CRC64;
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01-DEC-2001
01-OCT-2003
Ephrin B1.
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HSSP; P52800; 1IKO.
Ensembl; ENSDARG00000007723; Danio rerio.
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MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
Chan J. Mably J.D. Serluca F.C., Chen J.N., Goldstein N.B.,
Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.P.
"Morphogenesis of prechordal plate and notochord requires inta
eph/ephrin b signaling.",
Dev. Biol. 234:470-482(2001).
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Eukaryota; Metazoa; Chordata; (
Actinopterygii; Neopterygii; Topprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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                                                                                                                                                                                                                    LLLKLRKRTR----KHSQP----RGGTALSLSTLATPKGAAQAGSEPSDIIIPLR---TT
                                                                                                                                                                                                                                                                    AMCWRRRRAKPSESRHPGPGSFGRGGSL----
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                                                                                                             ENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY
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41.5%; Pred. No. 3.4e-31;
tive 49; Mismatches 109;
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US-11-186-284-39
US-11-186-284-31
US-11-186-284-31
US-11-186-284-31
US-10-821-234-1182
US-10-821-234-131
US-10-821-234-131
US-10-821-234-131
US-11-186-284-28
US-10-821-234-191
US-11-186-284-28
US-10-995-561-911
US-11-995-561-911
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Sequence 35, Appl
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Sequence 914, App
Sequence 1182, Ap
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 390
LENGTH: 459
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PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/454,300
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
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                                              324 IVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLFPVQVITT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                              134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 KYRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zozulya, Sergey
Kertesz, Nathalie
Reddy, Ramachandra
Gill, Parkash
NAKTKPREEQYNSTYRVVSVL--TVLHQDWLNGKEYKC-KVSNKALPAPIEKT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                                                                                                  CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                -PFCPHYEKVSG-----
                                                                                                                                                                                                 RSSTTSPFVKPNPGSSTDGNSAGHSGNNILG-SEVDP-----BPKSCDKTHT 237
                                                                                                                                                                                                                                                                                                                                               HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEKVSGDYGHPVYIVQEMPPQSPANIYY 331
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                                                                                                                                                                                                                                                  RRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADP------
                                                                                                                                                                                                                                                                                                                                                                                                  DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQ------166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.4%; Score 451.5; DB 6; 29.5%; Pred. No. 3.3e-29; tive 47; Mismatches 115;
                                                                                                                                                                                                                                                                                                   --DASSAGSTRNKDPTRRPELE---
                                                                                                                                                   -----PVY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 129;
                                                                                                                                                                                                                                                                                                   --AGTNG----- 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/454,300
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 425
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 388
                                                                                                                                           Sequence 288, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 388, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
APPLICANT:
APPLICANT:
APPLICANT:
                                                                              APPLICANT:
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CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/454,432
PRIOR FILING DATE: 2003-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH FILE REFERENCE: VASG-P02-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Krasnoperov, Valery APPLICANT: Zozulya, Sergey
                                                                                                                            APPLICANT:
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                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 233
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                            254 RRAKPSESRHPGPGSFGRGGSLGLGGGGGMG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                             194 HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRR 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Conservative
                                                                                                                                                                                                                                                                                                                   RSSTTSPFVKPNPGSSTDGNSAGHSGNNILG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
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Gill, Parkash
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Kertesz, Nathalie
                     Gerritsen, Mary E.
                                       Gao, Wei-Qiang
                                                             Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                          Beresini, Maureen
                                                                                                      DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10949720 p. US20050249736A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.0%; Score 442; DB 6; 35.8%; Pred. No. 8.7e-29; ative 36; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                      -DASSAGSTRNKDPTRRPELE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76; Indels
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191

166

APPLICANT:
APPLICANT:

APPLICANT:

Godowski, Paul J. Gurney, Austin L. Goddard, Audrey

Smith, Victoria

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RESULT 5
US-10-220-824-8
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
                  SOFTWARE: Kopatentin 1.71
SEQ ID NO 8
                                                                                                                                                                                                                                                              Sequence 8, Application US/10220824
Publication No. US20050277603A1
GENERAL INFORMATION:
APPLICANT: Viromed Limited
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                    TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including TITLE OF INVENTION: gene encoding an anti-angiogenic protein or parts thereof FILE REFERENCE: OPF0208/PCT CURRENT APPLICATION NUMBER: US/10/220,824 CURRENT FILING DATE: 2002-08-30 PRIOR APPLICATION NUMBER: KR 2001-0000691 PRIOR PRIOR PRIOR APPLICATION NUMBER: KR 2001-0000691 PRIOR FILING DATE: 2001-01-05
                                                        PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
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ORGANISM: Homo Sapien
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LENGTH: 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059115
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/059117
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/059263 FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/059184 FILING DATE: 1997-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYYYISKPIHOHEDR-----CLRLKVTVSGKITHSPOAHDNPQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSADAAM 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%; Score 164.5; DB 6
27.7%; Pred. No. 1.2e-06;
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; ORGANISM: H
US-10-220-824-8
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                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 35
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Best Local Similarity
Matches 73; Conserv
                                     Matches
                                                                      Query Match
                                                        Best
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/381,988 PRIOR FILING DATE: 2002-05-20 NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOTEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Millennium Pharmaceuticals, APPLICANT: Berger, Allison
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                                                                                                                                 TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                  LENGTH:
                                                      Local
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/361,978 FILING DATE: 2002-03-05
169 QSPRG--GAV-PRKPVSEMPMERDRGAAHSLEPGKENLPG------DPTSNATSRGAE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    620 PGVGER-----GPPGPQGPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 PQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDL 111
                                                                                                                                                                    1496
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGPPQSPPNI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGAPGPAGARGESGLAGAPGPAGPPGPPGPPGPPGPGLPAGFDDMEGS-GGPFWSTARSA 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPPGPPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG--LESLQGGVCLTRGMKVLLRVGQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DG-PQGPPGL 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAEPGELGIALRGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - PRGFPGPPGPPGVPGLPGEPGRFGVNSSDVPGPAGLPGVP-----GREGPPGFPGLP 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPRGGAVPRKP--VSEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guillemette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kamatkar, Shubhangi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/11186284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thibodeau, Stephen N.
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 144.5; DB 6 ilarity 23.5%; Pred. No. 0.00049; Conservative 18; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US20050266493A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allison
                                   5.8%; Score 142.5; DB 7; 29.1%; Pred. No. 0.0007; ative 15; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tracy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GAADPPFCP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----REGPPGRTGQKGSLGEAGAPGHKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSESSMENT, PREVENTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -HYEKVSGDYGHPVYIV---Q
                                                                      Length 1496;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GPPGPS-----
                                       43;
                                       Gaps
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PRIOR FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR PILING DATE: 2001-12-10

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR APPLICATION NUMBER: US 60/381,988

PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

SOPTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MCMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
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Matches
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 744
TYPE: PRT
ORGANISM: Homo
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275 LGLGG-GGGMGPREAEPGELGIALRGGGAADP--PFCPHYEKVSGDYGHPVYIVQDGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660 GERGEQGPP 668
                                                                                                             242 VAGAGGAMCWRRRRAKPSESRHPG-----
                                                                                                                                                                                                187 ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL----G
                                                                                                                                                                                                                                          223 -----GDRGPKGLPGPQG-----LRGPKGDKGFGMPGAPGVKGP-
                                                                                                                                                                                                                                                                                     127 HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM 186
                                                                                                                                                                                                                                                                                                                                                                      67 PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGPRGDPGTLGPPGPVGERGAPGNRGF----PGSDGLPGPKGAQGERGPVGSSGPKGSQ
                                                                                                                                                                                                                                                                                                                                PPGPHGLPG-----IGKPGGPGLPGQPGPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QSPP 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP----GSFGRGG
                                                                IPGIG-----KPGQDGIPGQPGFPGGKGEQGLPGLPGLPGIGKPGFPGPKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDPGRPGEPGLPGARG-----LTGNPGVQGPEGKLGPLGAPGEDGRPGPPGSIGIKGQPG
                                                                                                                                                     ----PGMHGL-PGPVGLPGVGKPGVTGFPGPQGPLGKPGAPGEPGRQGPIGVPGVQGPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 142; DB 7; Length 744; Pred. No. 0.00034;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 126;
                                                                                                             --PGSFGRGGS
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CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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Best Local S
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-02992RNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo
417
                                    330
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                                                                                                                                                          312
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                                                                                                                                                                                                                                                                             187
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                                                                                                                                                                                                                                                                                                                                                                                                198 PPGPHGLPG-----IGKPGGPGLPGQPGPK-------------
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                                                                                                                                                                                                                                                                                                                                                       127 HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM 186
                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
GIVGPQGPP 425
                                                                                                                LGLGG-GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGP----
                                                                                                                                                                                               VAGAGGAMCWRRRRAKPSESRHPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG
                                    ---- PQSPP 334
                                                                           RGMGGVPGALGPR-GEKGPIGAPGIGG----PPGEPGLPGIPGPMGPPGAIGFPGPKGEG
                                                                                                                                                          IPGIG-----
                                                                                                                                                                                                                                   ----PGMHG-PPGPVGLPGVGKPGVTGFPGPQGPLGKPGAPGEPGPQGPIGVPGVQGPPG
                                                                                                                                                                                                                                                                           ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL----G
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Schlegel, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thibodeau, Stephen N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 142; DB 7; Length 744; ilarity 23.3%; Pred. No. 0.00034; Conservative 16; Mismatches 99; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tracy L.
                                                                                                                                                                                                                                                                                                                  -GDRGPKGLPGPQG-----
                                                                                                                                                       KPGQDGIPGQPGFPGGKGEQGLPGLPGPPGLPGIGKPGFPGPKGD
                                                                                                                                                                                                                                                                                                                      LRGPKGDKGFGMPGAPGVKGP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 122;
                                                                                                                                                                                                 ---PGSFGRGGS 274
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                                                                                                                       329
                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                      256
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RESULT 9 US-10-821-234-964

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APPLICANT: Thibodeau, Stephen N.

APPLICANT: Burgart, Lawrence J.

IIILE OF INVENTION: MCYEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: MCYELOS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: MCYELOS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: MCYELOS FOR IDENTIFICATION, AND

CURRENT APPLICATION MCYBER: US/11/186,284

CURRENT FILING DATE: 2005-07-21

PRIOR APPLICATION NUMBER: US/0/301,822

PRIOR APPLICATION NUMBER: US/0/301,822

PRIOR APPLICATION NUMBER: US/0/301,971

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR APPLICATION NUMBER: US 60/361,978
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US-11-186-284-33
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; ORGANISM: Homo sapiens
US-10-821-234-964
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 964
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APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Berger, Allison

APPLICANT: Guillemette, Tracy L.
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 33
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                                                     NUMBER OF SEQ ID NOS:
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Schlegel, Robert
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Pred. No. 0.00063;
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Matches
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SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1182
LENGTH: 1874
TYPE: PRT
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Publication No. US20050255114A1
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APPLICANT:
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
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TITLE OF INVENTION: Methods for Diagnosis
FILE REFERENCE: 821A
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APPLICANT: Stache-Crain, Birgit
                                                                                                                                                                                                                                                                                                                                                                                                     y Match 5.6%; Score 137.5; DB Local Similarity 25.5%; Pred. No. 0.0023; hes 79; Conservative 15; Mismatches 8
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                                                                      GL-GGGGGMGPREAEPGELGIALRGG-----GAADPPFCPHYEKVSGDYGHPVYIVQDGP
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US-10-821-234-914
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               TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTMARE: pt SEQ_genes Version 1.0
SEQ ID NO 1431
LENGTH: 1366
TYPE: PRT
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 914
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
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APPLICANT: Stache-Crain, Birgit
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CURRENT FILING DATE: 2004-04-07
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APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                       Andarmani, Sus
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o. US20050255114A1
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US-11-186-284-31
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                                                                                                                                                                    US-11-186-284-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/111 Publication No. US20050266493A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 31
                                                                                Matches
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%; Score 134.5; DB 6; Length 1366; Best Local Similarity 25.3%; Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029PZRNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR RPPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Millennium Pharmaceuticals, APPLICANT: Berger, Allison
                                                                                                                                                                                                              TYPE: PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                        ORGANISM: Homo Sapiens
                                                                                                    Local
321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PPHSGPGGV--RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
                                                                                                                                                                                                                              1366
                                                                             89; Conservative
                                                                                                    Similarity
                                     PPHSGPGGV--RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRPGP----IGPAGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSRGASGPAGVRGPNGDAGRPG--EPGLMGPRGLPGSP-GNIGPAGKEGPV---GLPGID 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAVPRKPVSEMPMERDRGAAHSLEP---GKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
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PGLPGPRGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGEPGSAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGGLALLILIGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLGLGGG-G
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Guillemette, Tra
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Schlegel, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monahan, John E.
                                                                           5.5%; Score 134.5; DB 7; 25.3%; Pred. No. 0.0027; ative 14; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches 114;
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                                                                                                                        DB 7; Length 1366;
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TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-28
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PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/11/186,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Berger, Allison
                                                                                                                                                                                                                                                                                             / Match 5.4%; Score 133; DB 7; Length 1464;
Local Similarity 25.8%; Pred. No. 0.0039;
1es 99; Conservative 19; Mismatches 128; Indels 13
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                                         107 PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT--REGLESLQGGVCL----TR 159
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                                                                                                                                             62 CP--RARPPGPHSSPNYEFYKLYLVGGAQGRRCE------APPAPNLLLTCDR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-----CEAPPAPNLLLTCDRPDLDLRF 113
                                                                                                                                                                                                                                                2 GPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                               GPP--GPIG-NVGAPGAKGARG-----SAGP-----PGATGFPGAAGRVGPP 886
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-----AGEKGSPGADGP------AGAPGTPGPQGIAGQRGVVGLPGQRGER 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAVPRKPVSEMPMERDRGAAHSLEP---GKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
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Monahan, John E.
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Kamatkar, Shubhangi
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No. US20050266493A1
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1130 GPSG------ASGPAGPRGPP 1144
                                              313 KVSGDYGHPVYIVQDGP--PQSPP 334
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                                                                                                                                                                                                                                                                                                                                               160 GMKVLLRVG-----QSPRGGAVPRKPVSEM------PMERDRGAAHSLE--PGKENLP 204
                                                                                                                                                GP-GSFGRGGSLGL-GGGGGMGPR-----EAEPGELGIALRGG-----GAADPPFCPHYE 312
                                                                                                                                                                                                                                             GDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHP 264
                                                                                                                                                                                                                                                                                                 GFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAPAAEGSPGRDGSP 1030
                                                                                               GPAGPAGPVGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQ 1129
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                                                                                                                                                                                                                                                                                                                                                                                     MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	v	4.	w	2	٠,	No.	Result
144.5	145	145	145.5	146	146.5	4	4	148	148.5	149	149	151.5	ū	154.5	159	166	167.5	169.5	170.5	175.5	176	179	214.5	•	604.5	620.5	623	628.5	Score	
5.9	5.9		•	•	•	•	•			٠	٠		٠	6.3	٠	٠	٠	6.9	7.0	7.2	7.2	•	8.8	٠.	٠.	5		25.7	Match	Query
438	931	674	305	675	1774	1492	1315	921	316	569	325	301	1670	1049	680	205	228	201	228	213	209	238	237	345	345	333	346	336	Length	
N	N	N	N	N	N	N	N	N	N	N	N	N	μ	۳	N	N	N	N	N	ស	N	N	N	N	N	N	N	2	BB	
\$53787	S13580	S13301	T20906	S20819	B56101	A40333	A56101	S42617	T20497	S42886	T32248	B31219	ССНU3В	CGBO7S	S31216	A36377	I58170	I38850	A57084	JE0322	A54984	I38849	T19914	I58406	I48780	I84743	S46993	49	ID	
collagen alpha cha	alpha		ical pr				alpha	alpl	ical pr	ì	hypothetical prote	collagen 2 - Caeno		lagen alpha 1 (collagen alpha 1(X	B61 protein precur	LERK-7 precursor -	numan	repulsive axon gui	- hu	ELF-1 protein prec	C)	hypothetical prote	2 - rat	Stral/Eplg2 protei	ransmem	elk ligand - human	hepatoma transmemb		

45	44	43	42	41	40	39	38	37	36	35	34	υ u	32	31	30
140	140	140.5	141	141	141	141.5	142	142	142	142	142.5	142.5	142.5	143	144
5.7	5.7	5.7	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5. 8	5.8	5.8	5.8	5.8	5.9
680	304	305	744	744	319	1466	1763	1029	744	614	1496	743	635	1747	1027
ب	N	N	ب	μ	N	μ	N	۳	N	N	ب	Н	N	N	2
CGHULD	T22482	T30165	S23298	A34246	T32250	CGHU7L	S16366	S21369	S15435	T33149	CGHU2V	S23779	A57131	A54121	S28774
collagen alpha 1 (hypothetical prot	hypothetical prot	collagen alpha 1 (alpha	hypothetical prote	collagen alpha 1(collagen alpha 2(collagen alpha 1 (hypothetical prote		collagen alpha 1 (collagen alpha 2(V	collagen alpha-4	collagen alpha ch

ALIGNMENTS

Db 307 YEKVSGDY	Qy 311 YEKVSGDY	Db 254 KYRRHRK	Qy 251 WRRRRAKP	Db 194 GRSSTTSP	Oy 191 GAAHSLEP	Db 134 DYYIISTS	Qy 134 DYYIIATS	Db 74 GQYEYYKV	Oy 74 PNYEFYKL	Db 17 GLLMVLCR	Qy 14 GALLLIGV	Query Match Best Local Similarity 41.0 Matches 137; Conservative	A; Gene: HTK	A;Cross-references: UN	A; Molecule type: mRNA A; Residues: 1-336 < RES>	A;Status: preliminary;	A; Reference number: I4	A; Title: Molecular clo	R; Bennett, B.D.; Zeigl	C;Accession: I49766	C; Date: 02-Jul-1996 #sequence revision	hepatoma transmembrane kinase ligand	149766
YEKVSGDYGHPVYIVQEMPPQSPANIYY 334	YEKVSGDYGHPVXIVQDGPPQSPPNIYY 338	KYRRHRKHSPQHTTTLSLSTLATFKRGGNNNGSEPSDVIIFLRTADSVFCPH 306	WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310	GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253	GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250	DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193	EGLESLQGGVCLTRGMKV	GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLMGLEFQKNK 133	PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133	GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKVDSKTV 73	WNSANKRFQAEGGYVLYPQIGDRL	25.7%; Score 628.5; DB 2; Length 336; 41.8%; Pred. No. 3.2e-37; 7ative 49; Mismatches 129; Indels 13; Gaps 5;		A;Cross-references: UNIPROT:P52800; UNIPARC:UPI0000020B55; GB:L38847; NID:g769677; PIDN:		A;Status: preliminary; translated from GB/EMBL/DDBJ	I49766; MUID:95199254; PMID:7534404	A; Title: Molecular cloning of a ligand for the BPH-related receptor protein-tyrosine king	R.Bennett, B.D.; Zeigler, F.C.; Gu, O.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews,		#sequence revision 02-Jul-1996 #text change 09-Jul-2004	(hase ligand - mouse	

RESULT 2
\$4693
elk ligand - human
elk ligand - human
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

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R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-A;Reference number: I49766; MUID:95199254; PMID:7534404
A;Accession: I84743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlc EMBO J. 13, 3757-3762, 1994
A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kina A;Reference number: S46993; MUID:94349923; PMID:8070404
A;Accession: S46993
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                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-333 < RES>
                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
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A; Residues: 1-346 < BEC>
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                                                                                                                              Query Match
Best Local S
Matches 133
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Best Local S
Matches 143
                                                                                                                                                                                                                                    Cross-references: GDB:438338; OMIM:600527
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                                                                                    GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNIYY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPULLLTCDRPDLDLRFTIKFQEYS
PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                            GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLASPKGGSGTAGTEPSDIIIPLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LLLLGVAGAGGA------MCWRRRRAKPSESRHPGPGSFGRGGSLGL
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                                                                                                                                                                                                                13q33-13q33
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                                                                                                                              25.3%; Score 620.5; DB 2; ilarity 40.5%; Pred. No. 1.1e-36; Conservative 52; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.4%; Score 623; DB 2 39.2%; Pred. No. 8e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
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                                                                                                                                Indels
                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                    GB:L38734; NID:g769675;
                                                                                                                                                                                                                                                                                                                                                                                                                               receptor protein-tyrosine kii
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                                                                                                                                                                          333;
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A;Cross-references: UNIPARC:UPI00000018AC;
R;Shao, H.; Lou, L.; Pandey, A.; Pasquale,
J. Biol. Chem. 269, 26606-26609, 1994
A;Title: cDNA cloning and characterization
A;Reference number: A55062; MUID:95014510;
A;Accession: A55062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stral/Eplg2 protein - mouse (Stral/Eplg2 protein - mouse) (,Species: Mus musculus (house mouse) (,Species: Mus musculus (house mouse) (,Cpace) (,Cp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA, A;Residues: 1-89, T', 91-345 <SHA>
A;Cross-references: UNIPARC:UPI000016CADF;
C;Genetics:
A;Gene: EPLG2
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A;Title: Genomic organization and chromosomal localization A;Reference number: A55507; MUID:95203867; PMID:7896266
A;Accession: A55507
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A; Residues: 1-345 <FLE>
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R;Fletcher, F.A.; Renshaw,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                       HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA
                                                                                                                                                                                          ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKY 129
                                                                                                                                                                                                                                     AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--
                                                                                                                                                                                                                                                                                                                                                                                       ALLLIGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS
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   AHSLEPGKENLPGDPTSNATSRGAEGP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                24.7%; Score 604.5; DB 2; 37.9%; Pred. No. 1.6e-35; tive 51; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:U07598
E.B.; Dixi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a ligand for the Cek5 PMID:7929389
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         -LPPPSMPAVAGAAGG-----LA
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submitted to the EMBL Data A; Reference number: Z19195 A; Accession: T19914
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A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutiona: A;Reference number: I58406; MUJD:95022634; PMID:7936648
A;Accession: I58406
                   A; Molecule type: DNA
A; Residues: 1-237 <WIL>
                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                            C; Accession: T1 R; Mortimore, B.
                                                                                                                                                                              hypothetical protein C43F9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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A; Residues: 1-345 < RES>
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C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58406
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A;Cross-references: UNIPROT:Q9U3M2; UNIPARC:UPI0000078016; EMBL:Z82262; PIDN:CAB54195.1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 ALLLLGVLGLVSGL--SLEPVYMNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLLGVAGAGGA-------MCWRRRRAKPSESRHPGPGSFGRGGSLGL----GG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPNYMGLEFKKY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
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                                                                                                                                                                                                                                                                                                                                                                                                            VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSLSTLASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKT-----ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--
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                                                                                                                      Library,
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                                                                                                                         November
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                                                                                                                                                                                15-Oct-1999 #text_change 09-Jul-2004
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A;Experimental source: c
C;Genetics:
A;Gene: CESP:C43F9.8
A;Map position: 4
A;Introns: 32/2; 96/3; 2
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A;Cross-references: GDB:438336; OMIM:601381
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and A;Title: neceptor 138849; MUID:95140419; PMID:7838529
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Pate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 138849
C;Accession: 138849
R;KOZlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.;
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity

    human

                                                                         127
                                                                                                               118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GYVLYPQIGDRLDLLCPRARPP
                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTDHVISVHIGDRVSIRCPKSDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                     RKPVSEMP-----PGKENLP 204
                                                                                                                                                     SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF
                                                                                                                                                                                 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                                                                                                                                             GPG-----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN
                                                                                                                                                                                                                                                    GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRRGIENPK--FAARTLKKDRDAEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPRGGAVPRKPVSEMPMERDRGAAHS 195
                                                                         QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
                                                                                                             QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE
EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEVGQ
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                                                                                                                                                                                                                                                                                                                        7.3%; Score 179; DB 2; 28.4%; Pred. No. 1.3e-05;
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                                                                                                                                                                                                                                                                                                        24;
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                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
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                                                                                                                                                                                                                                                                                                        ; 0B
                                                                                                                                                                                                                                                                                                                                            Length 238;
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                                                                                                                                                                                                                                                                                                        60;
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                                                                                                                                                                                                                                                                                                        Gaps
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                                                                           174
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PID

A54984 ELF-1 protein precursor - mouse N;Alternate names: Cek7 ligand

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C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P52801; UNIPARC:UPI0000020CE3; GB:U14941; NID:g558836; R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M. J. Biol. Chem. 270, 3467-3470, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 79, 157-168, 1994
A;Title: Identification and cloning of ELF-1, a developmentally A;Reference number: A54984; MUID:95007776; PMID:7522971
A;Accession: A54984
  皍
                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-213 <AAS>
                                                                                                                                                                                                                                                                                                                                                                  C;Accession: JE0322
C;Accession: JE0322
C;Accession: Jeohys. Res. Commun. 252, 378-382, 1998
Biochem. Blophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, Chromosal mapping, and tissue expression
A;Reference number: JE0322; MUID:99045414; PMID:9826538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence
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A;Cross-references: UNIPARC:UPI0000020CE3; CC;Superfamily: axon guidance signal protein C;Keywords: lipoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 270, 3467-3470, 1995
A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine A;Reference number: A55873; MUID:95181289; PMID:7876076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-209 < CHE >
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                                                                                                                                                                                                                                                                                                                                               A; Accession: JE0322
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Best Local S
Matches 58
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Best Local S
Matches 43
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                                                                                                                      33 VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                 43;
                                                                                                                                                                                    Similarity
                                                                                VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAPEPIFTSNSSCSGLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151
GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISAT 154
                                      QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence_revision 05-Feb-1999 #text_change
                                                                                                                                                                                    7.2%;
36.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
                                                                                                                                                               Score 175.5; DB 2;
Pred. No. 2e-05;
4; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 176; DB 2;
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:U14752;
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                                                                                                                                                                 Indels
                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                     GB:AJ007292; NID:g3688367;
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Accession: I38850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P52804; UNIPARC:UPI0000129C92; GB:X90377; NID:g1061113; C;Superfamily: axon guidance signal protein C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage E;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 82, 359-370, 1995
Cell 82, 359-370, 1995
A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal
A;Reference number: A57084; MUID:95360980; PMID:7634326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
A57084
                                                                                                                                        A;Cross-references: GDB:438337; OMIM:601380
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein
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                                                                                                                                                                                                      A; Gene: GDB: EPLG4
                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P52798; UNIPARC:UPI0000129C90; EMBL:U14188; NID:g642834;
                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-201 < RES>
                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
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Matches
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                                                                                Similarity
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LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGFHSSPNYEFYKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAGAAGGLALLLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPN-----GPLK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQ-QGDYHIDVCINDYLDVFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLLGVLGL-VSGLSLEP------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LATLIFLLAMLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTIKFQEYSPNLWGHEFRSHHDYYIIATS---DGTREGLESLQGGVCLTRGMKVLLRVGQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARPPGPHSSPNYEFYKLYLVG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PANSCMKTIGVHDRVFDVNDKVENSLEPADDTV---RESAEPSRG-ENAAQTPRIPIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ycoprotein; membrane protein; phosphatidylinositol linkage signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llarity 28.9%; Pr
Conservative 30;
                                                                Conservative
                                                              6.9%; Score 169.5; DB 2; 29.9%; Pred. No. 5.1e-05; ative 18; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 170.5;
28.9%; Pred. No. 5e
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                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                  Indels
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                                                                                                       201;
                                                                  55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.; Bonhoeffer,
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58170; GO1812
R;Winslow, J. W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, Neuron 14, 973-981, 1995
B61 protein precursor - human (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004 (;Accession: A36377 R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.
                                                                                                                       RESULT
A36377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P52803; UNIPARC:UPI0000129C93; GB:S77167; NID:g914184; R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K. submitted to the EMBL Data Library, May 1995
A;Reference number: G08477
A;Accession: G01812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Cloning of AL-1, a ligand for an Eph-related tyrosine A;Reference number: I58170; MUID:95267434; PMID:7748564 A;Accession: I58170
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A;Cross-references: GDB:568757; OMIM:601535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-228 <KOZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-228 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: UNIPARC:UPI0000129C93; EMBL:U26403; NID:g1019430; PIDN:AAB60377.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Alternate names:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              DHTSKGFKRWECNRPHSPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                      PADDTV---HESAEPSRG-ENAAQTPRIPSRL----LAILLFLLA 223
                                                                                                                                                                                                                                                                                                                  AIPDNGRRS------CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE
                                                                                                                                                                                                                                                                                                                                                              S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE
                                                                                                                                                                                                                                                                PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVDWPGYESCOAEGPRAYKRWVCSLPFGHVQPSEKIQRFTPFSLGFEFLPGETYYYISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 167.5; DB 2; llarity 28.8%; Pred. No. 8.1e-05; Conservative 29; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GSPGESGTSGWRGGDTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                ----GPLKFSEKFOLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCLLLL 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
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Collagen alpha 1(X) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; Ct
Bur. J. Biochem. 213, 99-111, 1993
A;Title: Intron-exon structure, alternative use of promoter and expression of the mouse (
A;Reference number: S31216; MUID:93238750; PMID:8477738
A;Accession: S31216
A;Accession: S31216
A;Molecule type: DNA
A;Residues: 1-60 < KON>
A;Cross-references: UNIPROT:Q05306; UNIPARC:UPI000016CBAA; EMBL:Z21610; NID:g49793; PIDN
D:R1ima. K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Cron
A;Molecule type: mRNA
A;Residues: 1-12, F', 14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L'
A;Cross-references: UNIPARC:UPI00001773E5
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Blochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse type A;Reference number: I48299; MUID:92267014; PMID:1587271
A;Accession: I48299
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-285,'A',287-680 <ELI>A;Residues: 1-285,'A',287-680 <ELI>A;Cross-references: UNIPARC:UPI0000026913; EMBL:X67348; NID:g50480; PIDN:CAA47763.1;
R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium A;Reference number: A36377; MUID:91042512; PMID:2233719
A;Recession: A36377
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-205 <HOL>
A;Cross-references: UNIPROT:P20827; UNIPARC:UPI0000129C89; GB:C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 385-450, 'K', 452-627 <ELA>
A; Cross-references: UNIPARC: UPI000016CBAB;
R; Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Gabiochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide A;Reference number: S28807; MUID:93143676; PMID:8424763
A;Accession: S28807
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S31216
                                                                                                                                                                                                                                                                                              A;Title: Characterization of the mouse type X collagen A;Reference number: S30127; MUID:93261348; PMID:8492743 A;Accession: S30127 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 9.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CLRLKVTVSGKITHSPQAHVNPQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: X63013; NID: g49795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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C;Species: Bos prinigenius taurus (cattle)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004
C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R;Fietzek, P.F.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehr Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The aminc A;Reference number: A02862; MUID:80026026; PMID:488906
A;Accession: A02862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'A;Cross-references: UNIPARC:UPI000016CCAC; EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibod A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Accession: S26397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: collagen alpha 1(VIII) chain; complement Ciq carboxyl-terminal homology C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT> F;553-679/Domain: complement Ciq carboxyl-terminal homology <CiQ>
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A;Title: The covalent structure of calf skin type III collagen.
A;Reference number: A38001; MUID:80026027; PMID:488907
                                                                                                                          A; Molecule type: protein A; Residues: 1-242 <FIE>
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A; Introns: 51/3
C; Superfamily: col
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C; Genetics:
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A;Residues: 'SDGYFSQ', 24-26,'KQ' <SUM>
A;Cross-references: UNIPARC:UPI00001773E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                     A; Cross-references: UNIPROT: P04258; UNIPARC: UPI0000173B8A
                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1(III) chain - bovine
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Best Local S
Matches 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVODGP-----PQSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRGPVGPVGAKGVPGHNGEAGPR-GEPGIPGTR----GPTGPPGVPGFPGSKGDPGNP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G--LVGPAGPPGA---RGARGPPGLDGKTGYPGEPGLNGPKGNPGLPGQKGDPGVGGTPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLLLGVAGAGGAMCWRRRRAKP---SESRHPG-----PGSFGRGGSLGLGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPGAPGA----KGERGPAG--HPGEPGLPGSP----GNMGPQGPKGIPGNHGIPGAKGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSPNIWGHEFRSHHDYYIIATSDGT----REGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PGEKGHPGSPG----IAGPPGAPGFGKQGLPGLRG----QRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGPP--GPSGVGRRGENGFPGQPGI------KGDRGFPGEMG-----
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                               II.
                                                                                                                                                                                                                                                                                       E.; Kuehn,
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F;15-1040/Region: helical
F;587-589/Region: cell attachment (R-G-D) motif
F;752-754/Region: cell attachment (R-G-D) motif
F;752-754/Region: cell attachment (R-G-D) motif
F;875-877/Region: cell attachment (R-G-D) motif
F;878-880/Region: cell attachment (R-G-D) motif
F;935-937/Region: cell attachment (R-G-D) motif
F;1041-1049/Region: cell attachment (R-G-D) motif
F;107,119,938,950/Modified site: 5-hydroxylysine (Lys) #st
F;107,950/Modified site: allysine (Lys) #status predicted
F;107/Binding site: carbohydrate (Lys) (covalent) #status exp
F;107/Binding site: carbohydrate (Lys) (covalent) #status exp
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A;Accession: A38003
A;Molecule type: protein
A;Residues: 572-808 < LAN>
A;Cross-references: UNIPARC:UPI0000173B8D
A;Cross-references: UNIPARC:UPI0000173B8D
A;Cross-references: UNIPARC:UPI0000173B8D
A;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A;Title: The covalent structure of calf skin type III collagen.
A;Reference number: A38004; MUID:80026030; PMID:488910
A;Accession: A38004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <hEN>
A;Residues: 87-106;1017-1029;1037-1049 <hEN>
A;Residues: 87-106;00173B90; UNIPARC:UPI0000173B91; UNIPARC:UPI0000173B92
A;Cross-references: UNIPARC:UPI0000173B90; UNIPARC:UPI0000173B91; UNIPARC:UPI0000173B92
C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are h;
C;Comment: The type III collagen molecule is a trimer of identical chains, linked to each
C;Comment: The type III collagen molecule is a trimer of identical chains, linked to each
C;Comment: The type III collagen molecule is a trimer of identical chains, linked to each
C;Comment: Collagen alpha 1(I) chain; fibrillar collagen carboxyl-reminal homology;
C;Keywords: collagen alpha 1(II) chain; glycoprotein; hydroxylysine; hydroxyprolir
C;Keywords: collagen alpha 1(III) chain; #status experimental <CAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 809-947 < IDEW2>
A;Cross-references: UNIPARC: UPI0000173B8E
R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A;Title: The covalent structure of calf skin type III collagen. VI.
A;Reference number: A38005; MUID:80026031; PMID:488911
A;Accession: A38005
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A; Residues: 243-422 <DEW1>
A; Cross-references: UNIPARC: UPI0000173B8B
A; Cross-references: UNIPARC: UPI0000173B8B
R; Bentz, H; Fietzek, P. P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 197
A; Title: The covalent structure of calf skin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Cross-link analysis of the C-telopeptide domain A;Reference number: S71946; MUID:96404897; PMID:8809038 A;Accession: S71946
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R;Lang, H; Glanville, R.W.; Fietzek, P.P.; Kuc
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850,
A;Title: The covalent structure of calf skin t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI0000173B8F A;Experimental source: skin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;1-14/Region: amino-terminal nonhelical telopeptide
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. 318, 497-503, 1996
                                                                                                                                                                                                                                                                60;
                                                                                                                                                                                                                                                                                               Similarity
                                                                LPGDPTSNAT - -
                                                                                                                              PAGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGGRGPPGPPGSNGNPGPPGSSGAPGKDG
                                                                                                                                                                                            PRGGAVPRKPVSEMPMERDRGA--
   PPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGPQGPPGAPGPLGIAG---
                                                                                                                                                                                                                                                                                           6.3%;
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                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                           Score 154.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                Mismatches
                                                             -SRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGA
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                                                                                                                                                                                                                                                                                               0.0036;
                                                                                                                                                                                                                                                                                                                          DB 1;
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